

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 16:19:15 ; Search time 5274 Seconds

(without alignments)  
10706.087 Million cell updates/sec

Title: US-09-655-272-1\_COPY\_284\_1477

Perfect score: 1194

Sequence: 1 atgcgcagcaccacactctct.....gagacaagcgctgcgggtg 1194

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_cm.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	100.0	1794	6	AX018705 Sequence
2	1194	100.0	1794	6	BD140670 Novel mam
3	1194	100.0	1795	10	AF056492 Mus muscu
4	1070.8	89.7	1194	10	AF302842 Rattus no
5	814.4	68.2	1182	6	AR221261 Sequence
6	814.4	68.2	1182	6	AX250709 Sequence
7	814.4	68.2	1218	6	AR221262 Sequence
8	814.4	68.2	1257	6	AX278168 Sequence
9	814.4	68.2	1408	6	AX278166 Sequence
10	814.4	68.2	1544	9	AF248242 Homo sapi
11	814.4	68.2	1730	9	AF259500 Homo sapi
12	814.4	68.2	2747	9	AF259501 Homo sapi
13	814.4	68.2	2772	9	AF247042 Homo sapi
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15	542	45.4	1500	9	BC033577 Homo sapi
16	498.4	41.7	568	10	AF259502 Rattus no
17	392	32.8	181489	10	AC120557 Mus muscu
18	392	32.8	223092	2	AC147519 Mus muscu
19	340.8	28.5	257210	2	AC098622 Rattus no

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21	259.4	21.7	3056	10	AF385401	AF385401 Rattus no
22	249.8	20.9	1614	6	AX393903	AX393903 Sequence
23	249.8	20.9	1632	6	AX319989	AX319989 Sequence
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26	249.8	20.9	2065	6	AX411765	AX411765 Sequence
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33	235.2	19.7	3291	10	AF385402	AF385402 Rattus no
34	234.8	19.7	174562	2	AC005848	AC005848 Homo sapi
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38	229.2	19.2	1993	6	AX018706	AX018706 Sequence
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# ALIGNMENTS

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LOCUS	Sequence 1 from Patent WO9945108.					
DEFINITION	AX018705					
ACCESSION	AX018705.1	GI:10042825				
VERSION						
KEYWORDS	Mus sp.					
SOURCE	Mus sp.					
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1					
AUTHORS	Pink, M., Honore, E., Duprat, F., Lesage, F. and Lazdunski, M.					
TITLE	Novel mechanically sensitive mammal potassium channel family activated by polyunsaturated fatty acids and their use particularly for screening medicines					
JOURNAL	Patent: WO 9945108-A 1 10-SEP-1999;					
FEATURES	FINK MICHEL (FR); HONORE ERIC (FR); DUPRAT FABRICE (FR); LESAGE FLORIAN (FR); CENTRE NAT RECH SCIENT (FR); LAZDUNSKI MICHEL (FR)					
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# ORIGIN

Query Match 100.0%; Score 1194; DB 6; Length 1794;  
Best Local Similarity 100.0%; Pred. No. 6.1e-259;  
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
BD140670 1794 bp DNA linear PAT 18-SEP-2002
LOCUS Novel mammalian potassium channel families having mechanical
DEFINITION sensitivity activated by polyunsaturated fatty acid, and method for
using them particularly for drug screening.
ACCESSION BD140670.1 GI:23235615
VERSION JP 2002505102-A/1.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1794)
AUTHORS Honore, E., Fink, M., Lazdunski, M., Lesage, F. and Duprat, F.
TITLE Novel mammalian potassium channel families having mechanical
sensitivity activated by polyunsaturated fatty acid, and method for
using them particularly for drug screening
JOURNAL Patent: JP 2002505102-A 1 19-FEB-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT OS Unidentified
PN JP 2002505102-A/1
PD 19-FEB-2002
PF 23-FEB-1999 JP 2000534640
PI 05-MAR-1998 FR 98/02725
PI ERIC HONORE, MICHEL FINK, MICHEL LAZDUNSKI, FLORIAN LESAGE, PI
FABRICE DUPRAT
PC C12N15/09, A61K31/7088, A61K38/00, A61K39/395, A61K48/
00, A61P5/00,
PC A61P9/00, A61P21/00, A61P25/00, A61P25/28, C07K14/705, C07K16/28,
PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, G01N33/ PC
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CC Topology: Linear;
CC Novel mammalian potassium channel families having mechanical
CC activated by polyunsaturated fatty acid, and method for using
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CC them
CC particularly for drug screening.
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FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1194; DB 6; Length 1794;
Best Local Similarity 100.0%; Pred. No. 6.1e-259;
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGCAGCACCACACTCTGCTGCGCTCTGCTGCGACTGCTGCTTACTTGGTATCTGGG 60
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DEFINITION AF056492  
ACCESSION AF056492  
VERSION AF056492.1 GI:3329456  
KEYWORDS Mus musculus (house mouse)  
SOURCE  
ORGANISM  
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AUTHORS Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M. and Lazdunski, M.  
TITLE A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids  
JOURNAL EMBO J. 17 (12), 3297-3308 (1998)  
MEDLINE 98292450  
PUBMED 9628867  
REFERENCE 2 (bases 1 to 1795)  
AUTHORS Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M. and Lazdunski, M.  
TITLE Direct Submision  
JOURNAL Submitted (01-APR-1998) Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Valbonne 06560, France  
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## ORIGIN

Query Match 100.0%; Score 1194; DB 10; Length 1795;  
Best Local Similarity 100.0%; Pred. No. 6.1e-259;  
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 4
AF302842 1194 bp mRNA linear ROD 27-DEC-2001
LOCUS Rattus norvegicus mechanosensitive tandem pore potassium channel
DEFINITION mRNA, complete cds.
ACCESSION AF302842
VERSION AF302842.2 GI:17981766
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1. (bases 1 to 1194)
AUTHORS Kim, Y., Bang, H., Ghatenco, C. and Kim, D.
```

## TITLE

Synergistic interaction and the role of C-terminus in the activation of TRAAK K<sup>+</sup> channels by pressure, free fatty acids and alkali

Pflugers Arch. 442 (1), 64-72 (2001)

21268499

11374070

2 (bases 1 to 1194)

Kim, Y. and Kim, D.

Direct Submission

JOURNAL

Submitted (05-SEP-2000) Physiology, Finch University of Health Sciences/The Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064, USA

3 (bases 1 to 1194)

Kim, Y. and Kim, D.

Direct Submission

Submitted (27-DEC-2001) Physiology, Finch University of Health Sciences/The Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064, USA

Sequence update by submitter

On Dec 27, 2001 this sequence version replaced gi:14334013.

Location/Qualifiers

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SEQUENCE 1 from Patent WO0168670.  
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Lazdunski, M., Lesage, F. and Maingret, F.  
Novel family of mechanically sensitive human potassium channels  
activated by polyunsaturated fatty acids and use thereof  
Patent: WO 0168670-A 1 20-SEP-2001;  
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Best Local Similarity 81.5%; Pred. No. 3.3e-173;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

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DEFINITION Sequence 3 from patent US 6426197.  
AR221262  
ACCESSION AR221262  
VERSION AR221262.1 GI:23328171  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1218)









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Db	1187	AGGCCCGGATCCGCTTTGCGCCCGCGAAGAGCT	CAGCGGCTTTCCGCGCCACGGGCTCG	1246
Qy	1021	GCTCTGATTATACCCCACTGAGAAATCTGGCC	TTCATCGACGAGTCTCTCAGACACGCGAGAGT	1080
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DEFINITION	Homo sapiens two pore K+ channel Kt4.1b mRNA, complete cds.			
ACCESSION	AF259501			
VERSION	AF259501.1	GI:13925517		
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ORGANISM	Homo sapiens			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 2747)			
AUTHORS	Ozaita,A. and Vega-Saenz de Miera,E.			
TITLE	Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-pore K+ channel gene KCNK4. Chromosomal localization, tissue distribution and functional expression			
JOURNAL	Brain Res. Mol. Brain Res. 102 (1-2), 18-27 (2002)			
REFERENCE	2 (bases 1 to 2747)			
AUTHORS	Ozaita,A. and Vega-Saenz de Miera,E.C.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-APR-2000) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA			

FEATURES source

**CDS**

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## ORIGIN

Query Match 68.2%; Score 814.4; DB 9; Length 2747;  
Best Local Similarity 81.5%; Pred. NO. 3e-173;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

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189	Db	GCCTGTGTTCGGGCCCTGGAGCAGACCCACGAGCAGCAGGCCAGAGGGAGCTGGGG	248
121	Qy	CATGGCCGAGACCAAGTTCTGAGGAGCAATCCCTGTGTGAGCCAGAGAGCCTTGGAGGAT	180
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181	Qy	TTCATCAAGCTCTGTGTGAAGCCCTCGGAGGGGGCGCAAAACCCAGAAACCAAGCTGGAC	240
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Qy	361	TGTATCTTCTATGCACTGGTGGGGATCCCACTGTTTGGGATGCTCTGCGCGGAGTCGGG	420
Db	499	TGCATCTTCTATGCGTGGTGGGATTCGCGCTGTTTGGGATCTTACTGCGAGGGGTGCGG	558
Qy	421	GACCGGTGGGTCTCTCTGCGCGGGGCATCGGCACATCGAAGCAATCTTCTTTGAAG	480
Db	559	GACCGGTGGGTCTCTCTGCGCCCATGGCATCGGTCACTTTGAAGCCATCTTCTTTGAAG	618
Qy	481	TGGCATGTGCCACCGGGGCTGGTGAGAGTCTGTCCGCACTGCTCTCTGCTGATTCGGC	540
Db	619	TGGCACTGTGCCACCGGAGCTAGTAAGAGTGTGTGCGCGATGCTTTTCTGCTGATCGGC	678
Qy	541	TGCTGTCTTTTGTCTCACTCTCTACCTTCTGTTCTCTACATGAGAGCTGGAGCAAG	600
Db	679	TGCTGTCTTTTGTCTCACGCCCATGTCGTGTTCTGCTATATGAGAGACTTGGAGCAAG	738
Qy	601	TTAGAAGCCATCTACTTTTGTATAGTGAATCTTCCACACTGTATAGGCTTTGGCGATTATGTA	660
Db	739	CTGAGGCCATCTACTTTTGTATAGTGAAGCTTACCACTGCGGTGCGGCTTTGGCGACTATGTG	798
Qy	661	CCCGCGATGGCAACGGGCGAGACTCTCCAGCTTACAGCGCTGCTGTGTGTTCTTGATC	720
Db	799	GC CGGCGCGGACCCCGAGCGAGACTCCCGGCGCTATCAGCGCTGTGTGTGTTCTGATC	858
Qy	721	TTGTTTGGCCTAGACTACTTCTCGCTCAGTGTCTCACCACCTACCGCAACTGGTTGCGAGCA	780
Db	859	CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACCTACCGCAACTGGCTGCGAGTA	918
Qy	781	GTGTCCTCCGCAACTCGGGCAGAGATGGTGGCTTAACGGCAAGCTGCTAGCTCGAC	840
Db	919	GTGTCCTCCGCACTTCGGGCGAGAGATGGGCGGCTTACCGGCTCAGGCTGCAGCTGGACT	978
Qy	841	GGCAGAGTCAGAGCGAGTCAACCGAGCAACTGGGCGGCGCGCGCGCGCGCGCGGAGAG	900
Db	979	GGCAGAGTCAGAGCGGCTGACCCAGCGAGCGCGGCGCGCGCGCGCGCGCGGAGAG	1038
Qy	901	GAGCAACCACTCTCTGCGCTCTCTTTTGGCGGCAACCGCTGCTGTGTTGTGAGCAGCGCGC	960
Db	1039	GAGCAGCACTGC-----TGCTCTCACCGGCTTCTCAGCGCGAGCGCTGGGCTGGG	1086
Qy	961	AGCGCGGCTCTCTGCGACCGCGAGAGGTTGAGACTCCGCTCCCGCGCGCGCGCGCTCA	1020
Db	1087	AGCGCGGCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG	1146
Qy	1021	GCTCTGATTTACCCAGTGGAGAACTTGGCTTTATTCGACGAGTCTCTGACACCGCAGT	1080
Db	1147	GCCTTGAATATCCAGCGAGAACTTGGCTTCTATCGACGAGTCTCTCGGATACGACAGC	1206
Qy	1081	GAGGTGGTGTGCTCTGCTGCGGCTCTCGGGGTGCGCGCGCGCGCGCGCGCGCGCGCGG	1140
Db	1207	GAGCGGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG	1266
Qy	1141	AAGCTTTCAGACCGCGGGGTCTCTGCGGAGTCTCCGAGCAAGCGCGTGCCTGGT	1194
Db	1267	AAGCCGTGCGGCGG	1320
RESULT 14			

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2005, 14:16:02 ; Search time 652 Seconds

(without alignments)  
9613.204 Million cell updates/sec

Title: US-09-655-272-1\_COPY\_284\_1477

Perfect score: 1194

Sequence: 1 atgcgcagcaccacactct.....gagacaagccgtgcgggtg 1194

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_23Sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1194	100.0	1794	2	Aaz10606 cDNA enco
2	814.4	68.2	1182	3	Aaa27105 Human h-T
3	814.4	68.2	1182	4	Aah78636 Human mec
4	814.4	68.2	1218	3	Aaa27106 Human h-T
5	814.4	68.2	1257	6	Aah99922 Nucleotid
6	814.4	68.2	1257	12	Adi27937 Human TWI
7	814.4	68.2	1260	12	Adh51640 Human 123
8	814.4	68.2	1408	6	Aah99921 Nucleotid
9	814.4	68.2	1408	10	Adk52549 Hematolog
10	814.4	68.2	1408	12	Adh51638 Human 123
11	814.4	68.2	1408	12	Adi27935 Human TWI
12	814.4	68.2	2772	10	Aad58498 Human pot
13	814.4	68.2	2772	12	Adp21365 Gene KCNK
14	811.4	68.0	3945	8	Abx91950 Human G p
15	811.4	68.0	3996	5	Aas08652 Human cDN
16	811.4	68.0	3996	5	Adq98525 DNA enco
17	811.4	68.0	3996	8	Abx91949 Human G p
18	811.4	68.0	3996	9	Adb48285 Novel hum
19	809.8	67.8	3945	5	Aas11984 Human cDN
20	612.6	51.3	1337	4	Aah78646 Human mec
21	343.4	28.8	1265	4	Abao9473 Human K c

22	253	21.2	432	12	ADL87195	Adl87195 DNA up-re
23	253	21.2	432	12	ADL87194	Adl87194 DNA up-re
24	249.8	20.9	1614	6	AAI72558	Aai72558 ORF of hu
25	249.8	20.9	1614	6	AAD27459	Aad27459 Human TRE
26	249.8	20.9	1632	6	AAD34451	Aad34451 Human TRE
27	249.8	20.9	1632	6	ABK27503	Abk27503 DNA enco
28	249.8	20.9	1870	10	ADe07404	Ado07404 Novel cod
29	249.8	20.9	2028	8	ADA05745	Ada05745 Human NOV
30	249.8	20.9	2028	12	ADN62909	Adn62909 Human NOV
31	249.8	20.9	2065	6	ABK49585	Abk49585 Human cDN
32	249.8	20.9	2730	6	ABZ11550	Abz11550 Human pol
33	249.8	20.9	2730	12	ADM44068	Adm44068 Novel hum
34	248.2	20.8	1644	6	ABN85879	Abn85879 Hypothala
35	229.2	19.2	1393	2	AAZ10607	Aaz10607 cDNA enco
36	229.2	19.2	1994	2	AAZ00040	Aaz00040 Mouse h-T
37	229.2	19.2	3580	3	AAI17497	Aai17497 Murine TR
38	223.4	18.7	2820	6	AAI44676	Aai44676 Human tra
39	220.8	18.5	1236	3	AAI17496	Aai17496 Human TRE
40	220.8	18.5	1246	2	AAZ00039	Aaz00039 h-TREX1 p
41	220.8	18.5	1246	2	AAZ00412	Aaz00412 Human TRE
42	220.8	18.5	2391	11	ADP03564	Adp03564 Human GPC
43	220.8	18.5	3300	2	AAZ11915	Aaz11915 Human pot
44	219.2	18.4	2130	4	AAS12169	Aas12169 Human pot
45	217.6	18.2	2130	4	AAS12182	Aas12182 Human pot

#### ALIGNMENTS

RESULT 1

AAZ10606  
ID AAZ10606 standard; cDNA; 1794 BP.

XX  
AC AAZ10606;

XX  
DT 18-NOV-1999 (first entry)

XX  
DE cDNA encoding a mechanically sensitive potassium channel protein TRAAK.

XX  
KW Mechanically sensitive potassium channel protein; TRAAK;  
KW polynaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease; ds.

XX  
OS Mus sp.

XX  
FH Key

XX  
FT CDS

XX  
FT Location/Qualifiers

XX  
FT 284..1480

XX  
FT /\*tag= a

XX  
PN WO945108-A2.

XX  
PD 10-SEP-1999.

XX  
PF 23-FEB-1999; 99WO-FR000404.

XX  
PR 05-MAR-1998; 98FR-00002725.

XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.

XX  
PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;

XX  
PI WPI; 1999-551038/46.

XX  
DR P-PSDB; AAY30647.

XX  
XX New mechanically sensitive potassium channel, used to screen for specific

XX  
PT modulators, potential therapeutic agents for heart and nervous system

XX  
PT disorders.

XX  
PS Claim 6; Fig 1; 40pp; French.

XX  
XX The present sequence encodes a mechanically sensitive potassium channel

CC protein designated TRAAK. The protein is activated by polyunsaturated  
CC fatty acids, particularly arachidonic acid, and by riluzole. The protein  
CC is used to screen for specific modulators which are useful for treating  
CC or preventing diseases of the heart and nervous systems in humans and  
CC animals, e.g. epilepsy, cardiovascular disease (arrhythmia),  
CC neurodegeneration (particularly where associated with ischemia or  
CC anoxia), abnormalities of hormone secretion and muscular disease. The  
CC protein itself may be used to treat these diseases. Antibodies specific  
CC for the protein are used to detect it in tissues, also as therapeutic  
CC inhibitors or activators  
XX  
SQ Sequence 1794 BP; 348 A; 574 C; 494 G; 378 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1194; DB 2; Length 1794;  
Best Local Similarity 100.0%; Pred. No. 4.5e-313;  
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCGCAGCACCACATCTCTGGCTCTGCTGGCACTGCTGCTTTACTTTGATCTGGG 60  
Db 284 ATGCGCAGCACCACATCTCTGGCTCTGCTGGCACTGCTGCTTTACTTTGATCTGGG 343  
Qy 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTTCAGAGCAGCAGGCTCAGAGAAATGGAT 120  
Db 344 GCTCTAGTGTTCAGGCTCTGGAGCAGCTTCAGAGCAGCAGGCTCAGAGAAATGGAT 403  
Qy 121 CATGGCCGAGACCACTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGGAT 180  
Db 404 CATGGCCGAGACCACTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGGAT 463  
Qy 181 TTCATCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGGCCAAACCCAGAAACACAGCTGACC 240  
Db 464 TTCATCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGGCCAAACCCAGAAACACAGCTGACC 523  
Qy 241 AATAGCAGCACCACATCATGCTTGAACCTGGAGGGGGGCCAAACCCAGAAACACAGCTGACC 300  
Db 524 AATAGCAGCACCACATCATGCTTGAACCTGGAGGGGGGCCAAACCCAGAAACACAGCTGACC 583  
Qy 301 ATCATCACTACCATCGGCTATGCAATATAGTCTTACACACAGATGCGGGGGCTCTCTTT 360  
Db 584 ATCATCACTACCATCGGCTATGCAATATAGTCTTACACACAGATGCGGGGGCTCTCTTT 643  
Qy 361 TGATATCTTATGACATCTGGTGGGATCCCACTGTGTGGGATGTGTGGGGAGTGGG 420  
Db 644 TGATATCTTATGACATCTGGTGGGATCCCACTGTGTGGGATGTGTGGGGAGTGGG 703  
Qy 421 GACCGGTGGGCTCTCTGCGCGGGGATCGGCACATCGAACAATCTTCTGAAG 480  
Db 704 GACCGGTGGGCTCTCTGCGCGGGGATCGGCACATCGAACAATCTTCTTGAAG 763  
Qy 481 TGGCATGTGCGCACCGGGGCTGGTGAAGATCTGTCCGAGTGTCTTCTGCTGATCGGC 540  
Db 764 TGGCATGTGCGCACCGGGGCTGGTGAAGATCTGTCCGAGTGTCTTCTGCTGATCGGC 823  
Qy 541 TGCTGTCTTTGTCTCACTCTCACTCTGCTGTGTCTTACATGAGAGAGCTGAGCAAG 600  
Db 824 TGCTGTCTTTGTCTCACTCTCACTCTGCTGTCTTACATGAGAGAGCTGAGCAAG 883  
Qy 601 TTAGAGCCATCTACTTTGTTATGATGACCTCACCACCTAGGCTTTGGCGATATGTA 660  
Db 884 TTAGAGCCATCTACTTTGTTATGATGACCTCACCACCTAGGCTTTGGCGATATGTA 943  
Qy 661 CCGGGGATGGCAGCGGCGAGAACTCTCCAGCCTTACCAGCGCTGTGTGTGTCTGGATC 720  
Db 944 CCGGGGATGGCAGCGGCGAGAACTCTCCAGCCTTACCAGCGCTGTGTGTGTCTGGATC 1003  
Qy 721 TTGTTGGGCTAGCTACTTTCGCTCTAGTGTCTCACCACATCGGCAACTGTTGGAGCA 780  
Db 1004 TTGTTGGGCTAGCTACTTTCGCTCTAGTGTCTCACCACATCGGCAACTGTTGGAGCA 1063  
Qy 781 GTGTCGCGCGGAACTCGGGCAGAGATGGGTGGCTAACGCGCAGAGCTGTAGCTGACC 840  
Db 1064 GTGTCGCGCGGAACTCGGGCAGAGATGGGTGGCTAACGCGCAGAGCTGTAGCTGACC 1123

Qy 841 GGCACAGTGCACAGCGGAGTGACCCAGCGAACTGGGCCCCAGCGCCCCAGAGAG 900  
Db 1124 GGCACAGTGCACAGCGGAGTGACCCAGCGAACTGGGCCCCAGCGCCCCAGAGAG 1183  
Qy 901 GAGCAACCACTCTGCGCTCTCTTTGCGGGACCCGCTGCTGTGTTGAGCCAGCGGC 960  
Db 1184 GAGCAACCACTCTGCGCTCTCTTTGCGGGACCCGCTGCTGTGTTGAGCCAGCGGC 1243  
Qy 961 AGGCGCGGCTCCCTCCACCCGCGAGAGAGTTGAGACTCCGTCGCGCCCCAGCGCTCA 1020  
Db 1244 AGGCGCGGCTCCCTCCACCCGCGAGAGAGTTGAGACTCCGTCGCGCCCCAGCGCTCA 1303  
Qy 1021 GCTCTGATTTACCCAGTGCAGATCTGGCCTTCATGACGAGTCTCAGACAGCAGT 1080  
Db 1304 GCTCTGATTTACCCAGTGCAGATCTGGCCTTCATGACGAGTCTCAGACAGCAGT 1363  
Qy 1081 GAGCGTGGCTGTCCTGCTGCGGCTCTCTGCGGGTCTGCGGGTCCGCGAGCCCAACCCATCAAA 1140  
Db 1364 GAGCGTGGCTGTCCTGCTGCGGCTCTCTGCGGGTCTGCGGGTCCGCGAGCCCAACCCATCAAA 1423  
Qy 1141 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTCCGAGACAAAGCCCTGCGCGTG 1194  
Db 1424 AAGCCTTCCAGACCCCGGGTCTCTGGCGACTCCGAGACAAAGCCCTGCGCGTG 1477  
RESULT 2  
AA27105  
ID AAA27105 standard; cDNA; 1182 BP.  
XX  
AC AAA27105;  
XX  
DT 04-AUG-2000 (first entry)  
XX  
DE Human h-TRAAK cDNA sequence #1.  
XX  
KW Human; h-TRAAK; potassium channel polypeptide;  
KW 2P domain potassium channel; neurodegenerative disease; stroke;  
KW psychiatric disorder; neurological disorder; Gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1182  
FT /tag= a  
FT /product= "h-TRAAK protein #1"  
XX  
PN WO200026253-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-GB003634.  
XX  
PR 03-NOV-1998; 98GB-00024048.  
PR 07-OCT-1999; 99GB-00023668.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Chapman CG, Duckworth DM;  
XX  
XX WPI; 2000-365583/31.  
DR P-PSDB; AAY94425.  
XX  
PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
PT family of polypeptides, useful for the diagnosis and treatment of h-TRAAK  
PT related disorders, e.g. depression and schizophrenia.  
XX  
PS Claim 5; Page 21; 35pp; English.  
XX  
CC Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK  
CC polynucleotides from human tissue samples. h-TRAAK polypeptides have  
CC homology to the 2P domain potassium channel family of polypeptides. The h  
CC -TRAAK polypeptides and polynucleotides may be used in diagnostic assays  
CC for conditions related to h-TRAAK imbalance and for identifying agonists



CC and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and  
CC polynucleotides may also be useful for treatment and prevention (e.g. as  
CC vaccines) of certain diseases, such as pain, psychiatric disorders  
CC including depression and schizophrenia, neurodegenerative disease  
CC including Alzheimer's, stroke and head trauma and neurological disorders  
CC including migraine and epilepsy. The present sequence is human h-TRAAK-1  
CC cDNA sequence #1  
XX  
SQ Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other;  
Query Match 68.2%; Score 814.4; DB 3; Length 1182;  
Best Local Similarity 81.5%; Pred. No. 3.2e-210;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;  
QY 1 ATGCGAGCACCACATCTCTGGCTCTGCTGGCACTGGTCTTACTTGGTATCTGGG 60  
DB 1 ATGCGAGCACCACATCTCTGGCTCTGCTGGCACTGGTCTTACTTGGTATCTGGT 60  
QY 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCCTCAGAGCAGCAGGCTCAGAGAAATGGAT 120  
DB 61 GCGCTGTGTTCGGGGCCCTGGAGCAGCAGCAGCAGCAGCAGGAGGAGCTGGGG 120  
QY 121 CATGGCCGAGACCACTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGGAT 180  
DB 121 GAGGTCGAGAGAGAGTCTCTGAGGGGCCATCCGTGTGTGAGCAGCAGGAGCTGGGCCCTC 180  
QY 181 TTCTATCAAGCTCTCTGGTGTGAAGCCCTGGGAGGGGGCGCAACCCAGAAACCACTGGACC 240  
DB 181 CTCATCAAGGAGGTGCTGATGCTCCCTGGGAGGGGGTGGGACCCAGAAACCACTGGACC 240  
QY 241 ATAGCAGCAACCACTCATCAGCTTGGAACTGGGAGGCGCTCTCTTTCTCGGGGACC 300  
DB 241 AGCAACAGCAGCCAC---TCAGCTTGGGACCTGGGAGGCGCTCTTTCTCAGGGACC 297  
QY 301 ATCATCACTACCATCGCTATGCAATAGTCTTACACACAGATCGGGGGCTCTCTTT 360  
DB 298 ATCATCACACCATCGCTATGCAATAGTGGCCCTGGGACAGATGCGGGGCCCTCTTC 357  
QY 361 TGTATCTTCTATGCACTGTGGGGATCCCACTGTTCGGGATGCTGTGGCGGAGTCCGG 420  
DB 358 TGCATCTTTATGCGCTGTGGGATTCGCTGTGTGGGATCCTACTGGCAGGGGTCCGG 417  
QY 421 GACCGGTGGGCTCTCTCTGCGCGGGGAGATCGGCGACATCGAAGCAATCTTCTTGAAG 480  
DB 418 GACCGGTGGGCTCTCTCTGCGCGGATGGCATCGGTACATTAAGGCCATCTTCTTGAAG 477  
QY 481 TGGCATGTGCCACCGGGCTGTGAGAGTCTCTCGCAGTGTCTTCTGTGTATCGGC 540  
DB 478 TGGCAGGTGCCACCGGAGCTAGTAAGAGTGTCTGCGCGATGCTTTCTCTGTATCGGC 537  
QY 541 TGCTGTCTTGTCTCTCACT 600  
DB 538 TGCTGTCTTGTCTCTCACT 597  
QY 601 TTAGAAGCCATCTCTTTGTATGAGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 660  
DB 598 CTGGAGGCCATCTACTTTGATAGTACGCTTACCACCGCTTGGGCTTGGGAGTATGTG 657  
QY 661 CCGCGGATGGCAGCGGAGAGTCTCTCAGCGCTTACCGCGCTGTGTGTGTGTGTGTGT 720  
DB 658 GCGCGGCGGAGCCCGAGGAGGAGTCTCTCAGCGCTTACCGCGCTGTGTGTGTGTGTGT 717  
QY 721 TTGTTTGGCTAGCTACTTCTGCTCTAGTGTCTCTCAGCAGTCTCTCTCTCTCTCTCTCT 780  
DB 718 CTGCTCGGCTGTCTTCT 777  
QY 781 GTCTCCGCGCACTCGGCGAGAGATGGGTGGCTTAACCGGCAAGGCTGTCTAGCTGGACC 840  
DB 778 GTGTCCGCGCACTCGGCGAGAGATGGGCGGCTCTACGCGCTCAGGCTGCGAGTGGACT 837  
QY 841 GGCACAGTGAACGCGGAGTGAACCGAGCACTGGGGCCAGCGCCCGCGCCAGAGAG 900  
DB 838 GGCACAGTGAACGCGGCGTGAACCGAGCACTGGGGCCAGCGCCCGCGCCCGCGGAGAG 897

QY 901 GAGCAACCACTCTCTGCTCCCTCTCTTTGCGGCGACCGCTGTGTGTGAGCCAGCCGGC 960  
DB 898 GAGCAGCCACTGC-----TGCTTCCACCGCTGTGTGAGCCAGCCGGCTGGGC 945  
QY 961 AGSCCGGCTCCCTGTCACCGCAGAGAGGTTGAGACTCCGTCCCGCCCGCCAGGCTCA 1020  
DB 946 AGSCCGGCTCCCTGTCACCGCAGAGAGGTTGAGACTCCGTCCCGCCCGCCAGGCTCG 1005  
QY 1021 GCTCTGGATTACCCAGTGAAGATCTGGCTTTCATCGACGAGTCTCTCAGACGAGAGT 1080  
DB 1006 GCGCTGATTATCCAGCAGAGAACCTGGCTTTCATCGACGAGTCTCTCGGATACGAGAGC 1065  
QY 1081 GAGCGTGGTCTGCTCTGCGGCTCTCTGCGGCTCTCTGCGGCTGCGCGGAGCCCAACCCATCAAA 1140  
DB 1066 GAGCGGCTGCTGCTGCTGCGGCTCTCTGCGGCTGCGCGGAGAGTCTGCGGCTCAAAATCCCGCAGG 1125  
QY 1141 AAGCTTTCAGACCCCGGGGCTCTGCGGCTCTCTGCGGCTCTCTGCGGCTCTCTGCGGCTG 1194  
DB 1126 AAGCGCTGCGGCTCTGCGGCTCTCTGCGGCTCTCTGCGGCTCTCTGCGGCTG 1179  
RESULT 3  
AAH78636  
ID AAH78636 standard; cDNA; 1182 BP.  
XX  
AC AAH78636;  
DT 10-DEC-2001 (first entry)  
XX  
DE Human mechanically sensitive potassium channel hTRAAK cDNA.  
XX  
KW Human; mechanically sensitive potassium channel; riluzole; TWICK;  
KW polyunsaturated fatty acid; arachidonic acid; hTRAAK; chromosome 11q13;  
KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;  
KW hormone secretion; cardiac disease; vascular disease; ischemia;  
KW nervous system disorder; endocrinal disease; muscle disease;  
KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1182  
FT /tag= a  
FT /product= "mechanically sensitive potassium channel  
FT hTRAAK"  
XX  
PN WO200168670-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 14-MAR-2001; 2001WO-FR000758.  
XX  
PR 14-MAR-2000; 2000FR-00003264.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
PI Lazdunski M, Lesage F, Maingret F;  
XX  
DR WPI; 2001-590037/66.  
DR P-PSDB; AAG67777.  
XX  
PT New mechanically sensitive potassium channel, useful for treating  
PT cardiovascular diseases and in drug screening, is activated by  
PT polyunsaturated fatty acids.  
XX  
PS Claim 4; Page 32-33; 37pp; French.  
XX  
CC The present sequence encodes a human mechanically sensitive potassium  
CC channel which is activated by polyunsaturated fatty acids (particularly  
CC arachidonic acid (AA)) and by riluzole. The polypeptide is designated  
CC human TWICK-related AA-activated potassium channel (hTRAAK). The hTRAAK  
CC gene is located on chromosome 11q13. hTRAAK is involved in regulation of

CC neuronal and muscle excitation, cardiac rhythm and secretion of hormones.  
 CC Cells that express hTRAAK, designated to screen for modulators of hTRAAK  
 CC activity. Such modulators are potentially useful for prevention or  
 CC treatment, in humans and animals, of: cardiac and/or vascular disease;  
 CC nervous system disorders associated with ischemia and anoxia; endocrinal  
 CC diseases associated with anomalous hormone secretion or muscle diseases;  
 CC and retinal diseases. Typical examples are epilepsy, cardiac arrhythmia  
 CC and neurodegeneration  
 XX  
 XX Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other

Db	838	GGCACAGTGCACGCGCGGTGACCCAGCAGCGCGGCCCGCGCCCGCGCGAGAG	857
QY	901	GAGCAACCACTCTCTGCCCTCTTTTTCGCGGCACCGCTGCTGTTGTTGAGCAGCCGCGC	960
Db	898	GAGCAGCACTG-----TGCCTCCACCCCTGTCTCAGCGCAGCCGTGGGC	945
QY	961	AGSCCGGCTCCCTGCACCCGCGAGAGAGTTGAGACTCCGTCGCCGCCACCGGCTCA	1020
Db	946	AGSCCCCGATGCCCTCTTGCCCCCGAGAGAGCTCAGCGCTTCCCGCCACCGGCTCG	1005
QY	1021	GCTCTGGATTACCCCAAGTGAGAACTCTGGCTTCATCGACGAGTCTCAGACACGCAAGT	1080
Db	1006	GCCCTGGATTATCCACGCGAGAACTCTGGCTTCATCGACGAGTCTCGGATACGCAAGC	1065
QY	1081	GAGCTGGCTGTGCTTGCCTCGGCTCTCTCGGGTCGCGCGACCCACCCATCCAA	1140
Db	1066	GAGCGGGCTGCGCTGTGCCCGCGCGCAGAGTTCGCGCGCCCAATCCCCCAGG	1125
QY	1141	AAGCCTTCAGACCCCGGGGTCTCTGGCGGACTCCGAGACAAGGCGCTGCGGTG	1194
Db	1126	AAGSCCGTGGCTTCGCGGCCCTCGGGCTCTCCCGAGACAAGGCTGCGGTG	1179

**RESIST 4**

AA027106	AA027106	standard; cDNA; 1218 BP.
XX	XX	
XX	AA027106;	
XX	XX	
DT	04-AUG-2000	(first entry)
XX	XX	
DE	Human h-TRAAK cDNA sequence #2.	
XX	XX	
KW	Human; h-TRAAK; potassium channel polypeptide;	
KW	2P domain potassium channel; neurodegenerative	
KW	psychiatric disorder; neurological disorder; G	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
CD	37.1218	
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FT	/product= "h-TRAAK protein #2"	

Novel isolated h-TRAAK polypeptides belonging to the potassium channel family of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders, e.g. depression and schizophrenia.

Claim 11; Page 21 and 22; 35pp; English.

Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as



PT and cancer.

PS Claim 1; Page 122-124; 124pp; English.

This invention relates to a human TWIK-8 (tandem of P domains in a weak inward rectifying K<sup>+</sup> channel)-related potassium channel subunit polypeptide. Applications of the polypeptide include: neurotropic, neuroprotective, antiparkinsonian, antiarteriosclerotic, cytostatic, hypotensive, antidepressant, antimigraine, analgesic, vasotropic, anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene therapy, and as a modulator of potassium channel mediated activity in a cell, and is useful in screening assays, detection assays, predictive medicine and in methods of treatment. The polypeptide is useful as a target for developing modulating agents to regulate a variety of cellular processes, and is also useful as query sequence to perform a search against public databases to, for example, identify other family members or related sequences. The polypeptide is useful for treating disorders characterized by insufficient or excessive production of TWIK-8 protein or production of TWIK-8 protein forms which have decreased, aberrant or unwanted activity compared to TWIK-8 wild type protein, e.g., potassium channel associated disorders including central nervous system disorders such as cognitive and neurodegenerative disorders, autonomic function disorders, learning or memory disorders, cardiac disorders, muscular disorders, pain disorders and disorders of cellular growth, differentiation or migration. The polypeptide is useful as immunogen to raise anti-TWIK-8 antibodies, and to screen for drugs, and is also considered useful for producing non-human transgenic animals. This sequence represents the nucleotide sequence for human TWIK-8, which differs to the sequence in AAH99922 since it does not contain the 3' untranslated region

Sequence 1257 BP; 188 A; 443 C; 404 G; 222 T; 0 U; 0 Other;

Query Match	68.2%	Score 814.4;	DB 6;	Length 1257;
Best Local Similarity	81.5%;	Pred. No. 3.2e-210;		
Matches 973;	Conservative	0;	Mismatches 206;	Indels 15;
				Gaps 2;

1	QY	ATGGCGAGCACCACTCTGGCTCTGCTGGCACTGGTGTGCTCTTTACTTGGTATCTGGG	60
79	Db	ATGGCGAGCACCAAGCTCTGGCCCTCTGGCGCTGTCTTGTCTTAACTTGGTGTCTGGT	138
61	QY	GCTCTAGTGTTCAGAGTCTGGAGCAGCTCACAGCAGCAGGCTCAGAAGAAAATGGAT	120
139	Db	GCCTGTGTTCGGGCCCTGGAGCAGCCCAACAGCAGCAGGCCCAGAGGGAGCTGGG	198
121	QY	CATGGCCGAGACCAAGTTTCTGAGGGAACATCCCTGTGTGAGCCAGAGAGCTCTGAGGAT	180
199	Db	GAGGTCCGAGAGAAGTTCTGAGGGCCCATCCGTGTGTGAGCGACCAAGGAGCTGGGGCTC	258
181	QY	TTCAATCAAGCTCTCTGTGTGAAGCCCTGGGAGGGGGCGAAACCCAGAGAAACCACTGGAC	240
259	Db	CTCATCAAGGAGTGGCTGATGCCCTGGGAGGGGTGGGNACCCAGAGAACCAACTCGACC	318
241	QY	AATAGCAGCAACCACTCATCAGCTTGGAACTGGGCAGCGCCTTCTTTTCTCGGGGACC	300
319	Db	AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGCAGCGCTTCTTTTCTCAGGGACC	375
301	QY	ATCATCACTACCACTCGGCTATGGCAATATAGTCTTTACACAGAGATCGGGGCGCTCTTTT	360
376	Db	ATCATCAACCACTCGGCTATGGCAATGTGGCCCTGGCAAGATCGGGGCGCTCTTTC	435
361	QY	TGTATCTTCTATGCATCGTGGGATCCCACTGTTCGGGATGTCTGTGGCGGGAGTCGGG	420
436	Db	TGCATCTTTTATGGCTGTGGGATTCGGCTGTTTGGGATCTCTACTTGGCAGGGGTGGG	495
421	QY	GACCGGTGGCTCCTCTCTGCGCGGGGACATCGGCCACATCGAGCAATCTTCTTCGAG	480
496	Db	GACCGGTGGGCTCCTCCCTGGCGCATGGCATCGGTCACATTTGAAGCCATCTTCTTGAG	555
481	QY	TGGCATGTGCCACCGGGGCTGGTGAGAACTGTCTCGCAGTGTCTTCTCTGCTGATCGGC	540
556	Db	TGGCAGTGTCCACCGGAGCTAGTAGAGTGTGTTCGGCGATGCTTTTCTCTGCTATCGGC	615





QY 781 GTGTCCCGCGAAGTCTCGGCGAGAGATGGTGGGCTTAACGCGACAGGCTGTAGCTGGACC 840  
 DB |||||  
 DB 856 GTGTCCCGCGCACTCGGCGAGAGATGGGCGGCTTACGGCTCAGGCTGCGAGTGGACT 915  
 QY 841 GGCACAGTGCACGGCGAGTACCCAGCGAATCTGGGCGCCAGCCCGCGCGCAGAGAG 900  
 DB |||||  
 DB 916 GGCACAGTGCACGGCGAGTACCCAGCGAGCCGCGCGCGCGCGCGCGCGAGAG 975  
 QY 901 GAGCAACCACTCTGCGCCCTCTCTTTGCGCGCACCGCTGCTGTGTTGAGCCAGCGCGC 960  
 DB |||||  
 DB 976 GAGCAGCACTGC-----TGCTTCCACCGCCCTGTCCAGCGAGCGCTGGGC 1023  
 QY 961 AGGCGCGGCTCCCTGTCACCGCGAGAGAGTGTAGACTCCGTCCCGCGCCACAGGCTCA 1020  
 DB |||||  
 DB 1024 AGGCGCGGATCCCTTTCGCGCCCGCGAGAGGCTCAGCGCGCTTCCCGCGCCAGCGCTCG 1083  
 QY 1021 GCTCTGATTAACCCAGTGAATCTGCGCTTCTATCGACAGTCTTATCGACAGCGAGT 1080  
 DB |||||  
 DB 1084 GCGCTGATTAATCCAGCGAGAACCTGGCTTTCATCGACAGTCTCTGGATACGCGAGC 1143  
 QY 1081 GAGCGTGGCTGTGCGCTGCTCGGCTCTCTCGGCTCGCGCGAGCCCAACCCATCCAAA 1140  
 DB |||||  
 DB 1144 GAGCGGCTGTGCGCTGCTCGGCTCGCGCGAGAGTCTCGCGCGCCCAATCTCCCCCAGG 1203  
 QY 1141 AAGCTTCCAGACCCCGGGTCTCTGGCGGACTCCGAGACAAAGCGCGTGCCTGGTG 1194  
 DB |||||  
 DB 1204 AAGCGCTGCGCGCGCGCGCGCGCGCTTCCCGAGACAAAGCGTGCCTGGTG 1257

RESULT 8  
 AAH99921  
 ID AAH99921 standard; cDNA; 1408 BP.  
 AC AAH99921;  
 XX  
 XX  
 DT 25-JAN-2002 (first entry)  
 DE  
 DE Nucleotide sequence of human TWIK-8 receptor channel.  
 XX  
 XX Human; potassium channel; transmembrane domain; TWIK; TWIK-8;  
 KW Tandem of P domain in a Weak Inward rectifying K<sup>+</sup> channel; K<sup>+</sup>;  
 KW central nervous system disorder; cardiovascular disease;  
 KW potassium channel mediated disorder; Alzheimers disease;  
 KW Parkinsons disease; multiple sclerosis; Picks disease;  
 KW neurodegenerative disorder; Lewy diffuse body disease; senile dementia;  
 KW Huntingtons disease; movement disorder; epilepsy; AIDS related dementia;  
 KW Gilles de la Tourettes syndrome; amyotrophic lateral sclerosis;  
 KW progressive supranuclear palsy; Jakob-Creutzfeldt disease;  
 KW autonomic function disorder; neuropsychiatric disorder; phobia;  
 KW bipolar affective disorder; ss; nootropic; neuroprotective;  
 KW antiparkinsonian; antiarteriosclerotic; cytostatic; hypotensive;  
 KW antidepressant; antimigraine; analgesic; vasotrophic; anticonvulsant;  
 KW neuroprotective; tranquilizer; neuroleptic; cancer;  
 KW learning and memory disorder; cell proliferation disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 84..1343  
 FT /\*tag= a  
 FT /product= "human TWIK-8"  
 XX  
 XX WO200177329-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-US011301.  
 XX  
 XX 07-APR-2000; 2000US-0195734P.  
 XX  
 XX (MILL-) MILLENIUM PHARM INC.  
 XX

Glucksmann MA;

WPI; 2002-010911/01.  
P-PSDB; AAG78406.

Novel isolated 12303, a human tandem of P domains in a weak inward rectifying potassium channel-related potassium channel subunit polypeptide useful for treating Alzheimer's disease, restenosis, migraine and cancer.

Claim 1; Fig 1; 124pp; English.

This invention relates to a human TWIK-8 (tandem of P domains in a weak inward rectifying K<sup>+</sup> channel)-related potassium channel subunit polypeptide. Applications of the polypeptide include: nootropic, neuroprotective, antiparkinsonian, antiarteriosclerotic, cytostatic, hypotensive, antidepressant, antimigraine, analgesic, vasotrophic, anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene therapy, and as a modulator of potassium channel mediated activity in a cell, and is useful in screening assays, detection assays, predictive medicine and in methods of treatment. The polypeptide is useful as a target for developing modulating agents to regulate a variety of cellular processes, and is also useful as query sequence to perform a search against public databases to, for example, identify other family members or related sequences. The polypeptide is useful for treating disorders characterized by insufficient or excessive production of TWIK-8 protein or production of TWIK-8 protein forms which have decreased, aberrant or unwanted activity compared to TWIK-8 wild type protein, e.g., potassium channel associated disorders including central nervous system disorders such as cognitive and neurodegenerative disorders, autonomic function disorders, learning or memory disorders, cardiac disorders, muscular disorders, pain disorders and disorders of cellular growth, differentiation or migration. The polypeptide is useful as immunogen to raise anti-TWIK-8 antibodies, and to screen for drugs, and is also considered useful for producing non-human transgenic animals. This sequence represents the nucleotide sequence for human TWIK-8

Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;

Query Match 68.2%; Score 814.4; DB 6; Length 1408;  
 Best Local Similarity 81.5%; Pred. No. 3 4e-210;  
 Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

QY 1 ATGCGCAGCACCACTCTCTGGCTCTGTGGCACTGGTGTCTTACTTGGTATCTGGG 60  
 DB |||||  
 DB 162 ATGCGCAGCACCACTCTCTGGCTCTGTGGCTGTGGTCTTACTTGGTGTCTGGT 221  
 QY 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTCAGCAGCAGCCTCAGAGAAATGGAT 120  
 DB |||||  
 DB 222 GCGCTGTGTTCGGGCGCTTGGAGCAGCCCGCAGCAGCAGCGGAGGAGTGGGG 281  
 QY 121 CATGGCCGAGACCAGTTCTGTAGGGACCATCCCTGTGTGAGCAGAGAGCTGGAGGAT 180  
 DB |||||  
 DB 282 GAGGTCCGAGAGAAATTTCTGAGGGCCCATCCGTGTGTGAGCAGCAGGAGCTGGGCTC 341  
 QY 181 TTCTATCAAGCTCCTGTGTTGAAGCCCTGGGAGGGGGCGCAAAACCCAGAAACAGCTGACC 240  
 DB |||||  
 DB 342 CTCATCAAGGAGGTGCTGATGCCCTGGGAGGGGGTGGGACCCAGAAACCACTCGACC 401  
 QY 241 ATAGCAGCAACCACTCATCAGCTTGGAACTGGGGCAGGCGCTTCTTTCTCGGGGACC 300  
 DB |||||  
 DB 402 AGCAACAGCAGCCAC---TCAGCTTGGGACCTGGGGCAGGCGCTTCTTTTCTCAGGACC 458  
 QY 301 ATCATCACTACCATCGGCTATGSCAATATAGTCTTACACACAGATCCCGGCGTCTCTTT 360  
 DB |||||  
 DB 459 ATCATCACCACCATCGGCTATGSCAATGTGGCCCTCGGCACAGATCCCGGCGCTCTTC 518  
 QY 361 TGTATCTTCTATGACTGGTGGGATCCCACTGTTCGGGATGTCTGGCGGAGTGGGG 420  
 DB |||||  
 DB 519 TGCATCTTTTATGCGCTGGTGGGATTCGCTGTGTGGGATCCTACTTGGCAGGGTGGG 578  
 QY 421 GACCGCTGGGCTCTCTCTGCGCGGGGATCGGCCACATCGAAGCAATCTTCTTGAAG 480  
 DB |||||





Db 342 CTGATCAGAGAGTGGTGATGCCCCGAGAGGGGGTGGGAGCCAGCAACCACTGACG 401  
Qy 241 AATAGCAGCAACCACTCATCAGCTTGGAACTGGGAGAGCGCTCTTTTCTCGGGAGCC 300  
Db 402 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGCAGCGCTCTTTTCTCAGGAGCC 458  
Qy 301 ATCATCACTACATCGGCTATGCAATATAGTCTTACACAGATCGGGGGTCTCTTT 360  
Db 459 ATCATCACCACCACTGGCTATGCAATATGCGCTGGCCTGGCAGATCGGGGGCTCTTC 518  
Qy 361 TGPATCTTCTATCACTGGTGGGATCCCACTGCTCGGATGCTGCTGGGGAGTCCGG 420  
Db 519 TGCATCTTTATGCGCTGGTGGGATTCGCTGTTTGGATCTCTATCGCAGGGGTCCGG 578  
Qy 421 GACCGCTGGGCTCTCTCTGCGCCGGGCACTCGGCCACATCGAACAATCTTTTGAAG 480  
Db 579 GACCGCTGGGCTCTCTCTGCGCCATGCGTACATGAGCCATCTTTTGAAG 638  
Qy 481 TGGCATGTGCCACCGGGCTGGTGAAGTCTGTCGCGAGTGTCTTCTGCTGATCGGC 540  
Db 639 TGGCAGTGGCCACCGGAGCTAGTAAGAGTGTCTGCGCGATGCTTTCTGCTGATCGGC 698  
Qy 541 TGCCTGCTCTTCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
Db 699 TGCCTGCTCTTCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 758  
Qy 601 TTAGAGCCATCTACTTTGTTATGAGTCTCTCACCACCTGTAGGCTTTGGCGATTATGA 660  
Db 759 CTGGAGCCATCTACTTTGTTATGAGTCTCTCACCACCTGTAGGCTTTGGCGATTATGA 818  
Qy 661 CCGCGGATGGCAACCGGCGAGAACTCTCAGCCTTACAGCGCTGTGTGTCTGTGATC 720  
Db 819 GCGCGGCGGACCGGCGAGAACTCTCAGCCTTACAGCGCTGTGTGTCTGTGATC 878  
Qy 721 TTGTTTGGCTAGCTTCT 780  
Db 879 CTGCTCGGCTGCTTCT 938  
Qy 781 GTCTCCCGGCACTCGGCGAGAGTGGTGGCTTAACGSCACAGGCTGTAGCTGGACC 840  
Db 939 GTCTCCCGGCACTCGGCGAGAGTGGGCGGCTCTCAGGCTCAGGCTGCGAGTGGACT 998  
Qy 841 GGCACAGTACAGCGGAGTGAACCGAGAACTGGGCGCAGCGCCCGCGCGCGAGAG 900  
Db 999 GGCACAGTACAGCGGCGTGAACCGAGAACTGGGCGCAGCGCCCGCGCGCGAGAG 1058  
Qy 901 GAGCAACCACTCTGCGCTCTCTTTGCGGCAACCGCTGCTGTTGAGCGCAGCGGC 960  
Db 1059 GAGCAGCACTGC-----TGCTTCCACCGGCTGTCCAGCGCAGCGCTGGGC 1106  
Qy 961 AGGCGCGGCTCCCTGCAACCGCGAGAGAGTTGAGACTCCGTCCTCCCGCCACGGCTCA 1020  
Db 1107 AGGCGCGGATCCCTTTCGCCCCCGAGAGGCTCAGCGGCTTCCCGCCACGGCTCG 1166  
Qy 1021 GCTCTGATTAACCGAGTGAATCTGGCCCTTATCGAAGTCTCTCAGACGCGAGAGT 1080  
Db 1167 GCGCTGATTAACCGAGAGAACTGGCCCTTATCGAAGTCTCTCGGATACGAGAGC 1226  
Qy 1081 GAGCGTGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
Db 1227 GAGCGGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1286  
Qy 1141 AAGCTTTCCAGAGCCCGGGGTCTCTGGGCGACTCCGAGACAAGGCGGCTGCGCGTG 1194  
Db 1287 AAGCGCGTGGCGTG 1340  
RESULT 10  
ADH51638  
ID ADH51638 standard; cDNA; 1408 BP.  
XX AC ADH51638;  
XX

DT 25-MAR-2004 (first entry)  
XX Human 12303 protein cDNA sequence.  
DE cytostatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;  
XX respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;  
KW immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;  
KW antianemic; endocrine-Gen; neuroprotective; nootropic; cardiant;  
KW gene therapy; cellular proliferative; differentiative disorder; brain;  
KW blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;  
KW pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;  
KW immune disorder; inflammatory disorder; cardiovascular disorder;  
KW endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesis;  
KW neoplastic; endocrine disorder; neurological; heart; tissue typing;  
KW chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;  
XX ss; 12303.  
OS Homo sapiens.  
XX US2003219806-A1.  
XX 27-NOV-2003.  
XX 18-MAR-2003; 2003US-00391399.  
XX 22-FEB-2000; 2000US-00510706.  
PR 07-APR-2000; 2000US-0195734P.  
PR 31-MAY-2000; 2000US-00583373.  
PR 26-JUN-2000; 2000US-0214176P.  
PR 08-AUG-2000; 2000US-00634669.  
PR 31-AUG-2000; 2000US-0229036P.  
PR 19-SEP-2000; 2000US-0233537P.  
PR 01-FEB-2001; 2001US-0267076P.  
PR 20-FEB-2001; 2001US-00789481.  
PR 12-MAR-2001; 2001US-0275078P.  
PR 12-MAR-2001; 2001US-0275172P.  
PR 06-APR-2001; 2001US-00828035.  
PR 26-JUN-2001; 2001US-00891762.  
PR 29-AUG-2001; 2001US-00942447.  
PR 17-SEP-2001; 2001US-0329883P.  
PR 19-SEP-2001; 2001US-00957683.  
PR 27-SEP-2001; 2001US-0325854P.  
PR 04-DEC-2001; 2001US-0336936P.  
PR 31-JAN-2002; 2002US-00062937.  
PR 08-MAR-2002; 2002US-00094214.  
PR 11-MAR-2002; 2002US-00095139.  
PR 17-SEP-2002; 2002US-00245121.  
PR 26-SEP-2002; 2002US-00255532.  
PR 04-DEC-2002; 2002US-00309804.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Glucksmann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;  
XX WPI; 2004-010868/01.  
XX P-PSDB; ADH51639.  
XX New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,  
XX 55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,  
XX useful for diagnosing, preventing or treating e.g. proliferative or brain  
XX disorders.  
XX Claim 1; SEQ ID NO 18; 276pp; English.  
XX This invention relates to novel human DNA sequences (designated 18607,  
XX 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,  
XX 52991, 59914, 59921 or 33751) and the proteins encoded by them. The  
XX invention may be useful for the development of compounds with a  
XX cytostatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen,  
XX respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,  
XX immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic,  
XX antianemic, endocrine-Gen, neuroprotective, nootropic or cardiant  
XX activity. In addition, the sequences may be useful for gene therapy. The

invention may be useful in diagnosing, preventing or treating disorders characterised by aberrant 18603, 15603, 49318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for example cellular proliferative and/or differentiative disorder, brain disorder, blood vessel disorder, platelet disorder, breast disorder, colon disorder, kidney disorder, lung disorder, ovarian disorder, prostate disorder, pancreatic disorder, skeletal muscle disorder, testicular disorder, hormonal disorder, disorder associated with bone metabolism, immune disorder, inflammatory disorder, cardiovascular disorder, endothelial cell disorder, liver disorder, viral disease, pain, metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder, endocrine disorder, neurological disorder or heart disorder. They may also be used in screening assays, tissue typing, chromosomal mapping, predictive medicine or pharmacogenomics. The present sequence is that of the cDNA which encodes the human 12303 protein of the invention.

XX SQ Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;

Query Match 68.2%; Score 814.4; DB 12; Length 1408;  
Best Local Similarity 81.5%; Pred. No. 3.4e-210;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

Qy 1 ATGCGAGCACCACATCTCTGGCTCTGCTGGCACTGGTGTCTTACTTGTATCTGGG 60  
Db 162 ATGCGAGCACCACGCTCTCTGGCTCTGCTGGCTCTGCTGGCTCTTACTTGTGTCTGT 221

Qy 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTCAGAGCAGCAGCTCAGAGAAATGGAT 120  
Db 222 GCTCTAGTGTTCAGGCTCTGGAGCAGCTCAGAGCAGCAGCTCAGAGAAATGGAT 120

Qy 121 CATGCGCGAGCAGCAGTCTCTGAGGAGCAGCTCTGCTGAGCAGCAGCAGCTGGAGAT 180  
Db 282 GAGTCTCGAGAGAGTCTCTGAGGAGCAGCTCTGCTGAGCAGCAGCAGCTGGGCTC 341

Qy 181 TTATCAAGTCTCTGGTGAAGCCCTGGAGGGGGCGCAAAACCCAGAAACAGCTGGAC 240  
Db 342 CTATCAAGAGGTGGCTGATGCTGGAGGGGGTGGAGCCAGAAACCAACTGGACC 401

Qy 241 AATAGCAGCAGCAGCAGTCTATGAGTGGAGCTGGAGCAGCAGCTCTTTCTGGGAGC 300  
Db 402 AGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 458

Qy 301 ATCATCACTACATCGGCTATGGCAATATAGTCTTACACAGATGCGGGGCTCTTTT 360  
Db 459 ATCATCACTACATCGGCTATGGCAATATAGTCTTACACAGATGCGGGGCTCTTTT 518

Qy 361 TGTATCTTATGACTGGTGGATCCCATGTTGCGGATGCTGCGGGAGTGGG 420  
Db 519 TGTATCTTATGACTGGTGGATCCCATGTTGCGGATGCTGCGGGAGTGGG 578

Qy 421 GACCGCTGGCTCTCTCTGCGCGGGGATCGGCCACATCGAAGCAATCTTCTGAAG 480  
Db 579 GACCGCTGGCTCTCTCTGCGCGGGGATCGGCCACATCGAAGCAATCTTCTGAAG 638

Qy 481 TGGCATATGCGCAACCGGGGCTGGTGAAGTCTGTCGAGTGTCTTCTGCTATCGGC 540  
Db 639 TGGCATATGCGCAACCGGGGCTGGTGAAGTCTGTCGAGTGTCTTCTGCTATCGGC 698

Qy 541 TGCCTGCTCTTGTCT 600  
Db 699 TGCCTGCTCTTGTCT 758

Qy 601 TTAGAAGCAGCAGTCT 660  
Db 759 CTGAGGAGCAGTCT 818

Qy 661 CCCGGGAGTGGCAGCGGAGCAATCTCTCAGCCTACAGCGCTGTGTGTCTTCTGATC 720  
Db 819 GCGCGGCGGAGCAGCGGAGCAATCTCTCAGCCTACAGCGCTGTGTGTCTTCTGATC 878

Qy 721 TTGTTTGGCTAGCT 780  
Db 879 CTGCTCGGCTGGCT 938

Qy 781 GTGTCCCGCCGAATCTCGGCGAGAGATGGGTGGCTTAACGGCAGAGGCTGTAGCTGAC 840  
Db 939 GTGTCCCGCCGCACTCGGCGAGAGATGGGCGGCTCAACGGCTCAGGCTGCGAGTGG 998

Qy 841 GGCACTGACAGCGGAGTGTACCCAGGAACTGGGCGGCGGCGGCGGCGGCGGCGG 900  
Db 999 GGCACTGACAGCGGAGTGTACCCAGGAACTGGGCGGCGGCGGCGGCGGCGGCGG 1058

Qy 901 GAGCAACCACT 960  
Db 1059 GAGCAGCACTGCT 1106

Qy 961 AGGCGCGGCT 1020  
Db 1107 AGGCGCGGCT 1166

Qy 1021 GCTCTGGATTAACCCAGTGAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080  
Db 1167 GCTCTGGATTAACCCAGTGAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1226

Qy 1081 GAGCGTGGCT 1140  
Db 1227 GAGCGGCT 1286

Qy 1141 AAGCCTTCCAGACCCCGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1194  
Db 1287 AAGCCTTCCAGACCCCGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1340

RESULT 11  
AD127935  
ID AD127935 standard; cDNA; 1408 BP.  
XX  
AC AD127935;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human TWIK-8 cDNA.  
XX  
KW Human; TWIK-8; gene; ss; ion channel family; ICF; cancer; leukaemia;  
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;  
KW hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;  
KW neurotropic; antiparkinsonian; hepatotropic; cardiovascular.  
XX  
OS Homo sapiens.  
XX  
PN US2003165891-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 15-MAY-2002; 2002US-00146733.  
XX  
PR 29-FEB-2000; 2000US-00515520.  
PR 29-FEB-2000; 2000US-0185938P.  
PR 03-MAR-2000; 2000US-00518866.  
PR 07-APR-2000; 2000US-0195734P.  
PR 11-APR-2000; 2000US-0195993P.  
PR 26-APR-2000; 2000US-0199799P.  
PR 19-SEP-2000; 2000US-0233537P.  
PR 25-SEP-2000; 2000US-0235018P.  
PR 25-SEP-2000; 2000US-0235059P.  
PR 15-DEC-2000; 2000US-0256240P.  
PR 18-DEC-2000; 2000US-0256588P.  
PR 21-DEC-2000; 2000US-0258028P.  
PR 28-FEB-2001; 2001US-00796720.  
PR 06-APR-2001; 2001US-00828035.  
PR 11-APR-2001; 2001US-00833081.  
PR 25-APR-2001; 2001US-00843128.  
PR 19-SEP-2001; 2001US-00957683.  
PR 25-SEP-2001; 2001US-00964252.  
PR 25-SEP-2001; 2001US-00964256.  
PR 17-DEC-2001; 2001US-00024623.

XX PA	(MILL-) MILLENNIUM PHARM INC.	
XX PI	Curtis RAJ, Gluckmann MA, Silos-Santiago I;	
XX XX	WPI; 2004-069000/07.	
DR DR	P-PSDB; ADI27936.	
XX XX	TIWK-6, TIWK-7, IC23927, TIWK-8, IC47611, IC47615, HNMDA-1, TIWK-9, PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and PT cardiovascular disorders.	
XX XX	Claim 1; SEQ ID NO 28; 638pp; English.	
PS PS	The invention relates to TIWK-6, TIWK-7, IC23927, TIWK-8, IC47611, CC IC47615, HNMDA-1, TIWK-9, alpha-2delta-4, 54414 and 53763 ion channel CC family (ICF) nucleic acids and proteins. The TIWK-6, TIWK-7, IC23927, CC TIWK-8, IC47611, IC47615, HNMDA-1, TIWK-9, alpha-2delta-4, 54414 and CC 53763 ICF nucleic acids and proteins may be used for preventing, CC diagnosing and treating ICF-related diseases. The sequences may be used CC to treat disorders associated with decreased expression by rectifying CC mutations or deletions in a patient's genome that affect the activity of CC ICF proteins by expressing inactive proteins or to supplement the activity CC of ICF proteins own production of ICF proteins. The proteins may also be used as CC antigens in the production of antibodies against ICF proteins and in CC assays to identify modulators of ICF protein expression and activity. The CC anti-ICF protein antibodies, agonists and antagonists may be used to CC regulate ICF protein expression and activity. The antibodies may also be CC used as diagnostic agents for detecting the presence of ICF proteins in CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This CC sequence represents cDNA encoding the human TIWK-8 protein of the CC invention. Note: The sequence data for this patent is also available in CC electronic format from USPTO at <a href="http://seqdata.uspto.gov/sequence.html">seqdata.uspto.gov/sequence.html</a> .	
XX SQ	Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;	
Query Match 68.2%; Score 814.4; DB 12; Length 1408;		
Best Local Similarity 81.5%; Pred. No. 3.4e-210;		
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;		
QY	1 ATGCGCAGCACCACTCTCTGGCTCTGCTGGCACTGGTGTCTTACTTTGGTATCTGGG 60	
DB	162 ATGCGCAGCACCACTCTCTGGCTCTGCTGGCACTGGTGTCTTACTTTGGTGTCTGGT 221	
QY	61 GCTCTAGTGTTCAGGCTCTGGAGCAGCTCTCAGCAGCAGGCTCAGAGAAATGGAT 120	
DB	222 GCCTGTGTTCGGGGCCCTGGAGCAGCCCAAGCAGCAGCAGCAGGAGGAGCTGGGG 281	
QY	121 CATGGCCGACACCACTTTCTGGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGGAT 180	
DB	282 GAGGTCCGAGAGAGTTCCTTGAGGGCCCATCCGTGTGTGAGCCAGGAGCTGGGGCTC 341	
QY	181 TTCTCAAGCTCTCTGGTTGAAGCCCTGGGAGGGGGCCAAACCCAGAAACCACTGGACC 240	
DB	342 CTCTCAAGAGGTGGCTGATGCCCTGGAGGGGGTGGGACCCAGAAACCACTGGACC 401	
QY	241 AATAGCAGCAACCACTCATCAGTGTGAACCTGGGAGCGCCCTCTTTTCTCGGGACC 300	
DB	402 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGAGCGCCCTCTTTTCTCAGGAGCC 458	
QY	301 ATCATCACTACCACTGGCTATGCAATATAGTCTTACACACAGATCGCGGGCTCTCTTT 360	
DB	459 ATCATCAACCACTGCGCTATGCAATATGCGCCCTGGGACAGATGCGGGCGCCCTCTTC 518	
QY	361 TGTATCTTCTATGCACTGGTGGGATCCCACTGTTCGGGATGCTGTGGGGAGTCGGG 420	
DB	519 TGCATCTTTTATGGCTGTGGGGATTCCTGCTGTTCGGGATCTTACTTGGCAGGGTCTGG 578	
QY	421 GACCGGTGGGCTCTCTCTGCGCGGGGATCGGCGCACATCGAAGCAATCTTCTTGAAG 480	
DB	579 GACCGGCTGGGCTCTCTCTGCGCCATGGAATCGGTACATTAAGGCCATCTTCTTGAAG 638	
QY	481 TGGCATGTGCCACCGGGGCTGGTGAAGAGTCTGTTCGCGCAGTCTCTTCTCTGTGATCGGC 540	
DB	639 TGGCAGCTGCCACCGGAGCTAGTAAGAGTCTGTTCGCGCATGCTTTCTCTGCTGATCGGC 698	
QY	541 TGGCTGCTCTTTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600	
DB	699 TGGCTGCTCTTTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 758	
QY	601 TTAGAGAGCATCTACTTTCTTATAGTACTCTCACCACCTGTAGGCTTTGGCGATTATGTA 660	
DB	759 CTGGAGGCACTTACTTTGTCTAGTGAGCTTTACCACTGAGGCTTTTGGCGACTATGTG 818	
QY	661 CCGCGGATGGCACCCCGGCGAGAACTCTCCAGCCTTACCAGCCGTGTGTGTCTCTGATC 720	
DB	819 GCGCGCGCGGACCCAGCAGGAGACTCCCGGCTTATCAGCCGCTGTGTGTCTGATC 878	
QY	721 TTGTTTGGCTTAGCTTACTTTCGCTCAGTGTCTCACCACCATCGGCAACTGGTTGCGAGCA 780	
DB	879 CTGCTCGGCTTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGCAACTGGTTGCGAGTA 938	
QY	781 GTGTCCCGCGGACTCGGCGAGAGATGGGTAAAGCGCTAACCGCAGGCTCTAGCTGAGCC 840	
DB	939 GTGTCCCGCGGCACTCGGCGAGAGATGGGTAAAGCGCTAACCGCAGGCTCTAGCTGAGCT 998	
QY	841 GGCACAGTCACAGCGGAGTGAACCCAGCGAACTTGGGCGCCAGCGCCCGCCGCGAGAGAG 900	
DB	999 GGCACAGTCACAGCGGCGCTGACCCAGCAGCGCGCGCGCGCGCGCGCGCGCGAGAG 1058	
QY	901 GAGCAACCACTCTCTGCTCTCTCTTTTTCGCGGCACTGGCTGTCTTTTGTAGCCAGCGCGC 960	
DB	1059 GAGCAGCCACTGCT 1106	
QY	961 AGCGCCGGCTCCCTCTCAGCCGCGAGAGAGTGTGAGACTCCGTCCTCCGCGCCAGCGGCTCA 1020	
DB	1107 AGCGCCGGCTCCCT 1166	
QY	1021 GCTCTGATTAATCCCACTGAGAACTTGGGCTTCTCATCGAGAGTCTCTCAGACGCGAGT 1080	
DB	1167 GCCTGATTAATCCCACTGAGAACTTGGGCTTCTCATCGAGAGTCTCTCAGACGCGAGC 1226	
QY	1081 GAGCGGTGTGTGCT 1140	
DB	1227 GAGCGGTGTGTGCT 1286	
QY	1141 AGCCTTCCAGACCCCGGGTCTCTGGGAGTCTCCGAGACAGCGCGCTGCGGTG 1194	
DB	1287 AAGCCGTGCGGCGGTG 1340	
RESULT 12		
AAD58498 standard; DNA; 2772 BP.		
ID	AAD58498	
XX	AC	AAD58498;
XX	AC	AAD58498;
DT	04-DEC-2003	(first entry)
XX	DE	Human potassium channel, KCNK4 DNA.
XX	XX	Human; urological disorder; urinary incontinence; gene therapy; cancer;
KW	KW	kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
KW	KW	urethra; overflow urinary incontinence; stress urinary incontinence;
KW	KW	nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
KW	KW	potassium channel; KCNK4; gene; ds.
OS	OS	Homo sapiens.
XX	XX	Location/Qualifiers
PH	Key	64..1323
FT	CDS	/*tag= a
FT	FT	











Db 2734 GAGCGGGTGGCCCGTGGCCCGCGCGCGAGAGGTGCGCGCGCCCAATCCCCCAGG 2793  
Qy 1141 AAGCCTTCCAGAGCCCGGGGTCTGGGCGACTCCGAGACAAGGCCCGTGCCG 1191  
Db 2794 AAGCCCGTGGCGCCCGCGCGCGCGCGTCCCCCGAGACAAAGGCCGTGCGG 2844

Search completed: February 2, 2005, 17:34:59  
Job time : 657 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	814.4	68.2	1182	4	US-09-432-470-1		Sequence 1, Appli
2	814.4	68.2	1218	4	US-09-432-470-3		Sequence 3, Appli
3	811.4	68.0	3996	4	US-09-620-312D-195		Sequence 195, App
4	249.8	20.9	2730	4	US-09-799-451-432		Sequence 432, App
5	229.2	19.2	1994	3	US-09-236-080-5		Sequence 5, Appli
6	220.8	18.5	1246	3	US-09-236-080-1		Sequence 1, Appli
7	220.8	18.5	3300	3	US-09-336-643A-82		Sequence 82, Appli
8	124.4	10.4	996	4	US-09-561-763-6		Sequence 6, Appli
9	124.4	10.4	996	4	US-09-431-367B-6		Sequence 6, Appli
10	124.4	10.4	1575	4	US-09-561-763-4		Sequence 4, Appli
11	124.4	10.4	1575	4	US-09-431-367B-4		Sequence 4, Appli
12	117.2	9.8	1497	4	US-09-561-763-3		Sequence 3, Appli
13	117.2	9.8	1497	4	US-09-431-367B-3		Sequence 3, Appli
14	117.2	9.8	3452	4	US-09-561-763-1		Sequence 1, Appli
15	117.2	9.8	3452	4	US-09-431-367B-1		Sequence 1, Appli
16	102.8	8.6	321	3	US-09-236-080-3		Sequence 3, Appli
17	102.6	8.6	939	4	US-09-561-763-9		Sequence 9, Appli
18	102.6	8.6	939	4	US-09-431-367B-9		Sequence 9, Appli
19	102.6	8.6	2287	4	US-09-561-763-7		Sequence 7, Appli
20	102.6	8.6	2287	4	US-09-431-367B-7		Sequence 7, Appli
21	102.6	8.6	2571	3	US-09-336-643A-80		Sequence 80, Appli
22	75.2	6.3	1882	4	US-09-814-915A-45		Sequence 45, Appli
23	75.2	6.3	1894	3	US-08-749-816-1		Sequence 1, Appli
24	75.2	6.3	1894	3	US-09-144-914-1		Sequence 1, Appli
25	74.2	6.2	2514	3	US-09-144-914-3		Sequence 3, Appli
26	58	4.9	1086	4	US-09-362-842-13		Sequence 13, Appli
27	56.2	4.7	2988	4	US-09-362-842-1		Sequence 1, Appli

361 TGATATCTTCTATGACTGTTGGGATCCCACTGTTTCGGGATGCTGTCGGGAGTCTGGG 420  
Db  
358 TGATATCTTCTATGACTGTTGGGATCCCACTGTTTCGGGATGCTGTCGGGAGTCTGGG 417  
Qy 421 GACGGGTGGGCTCTCTCTGCGCGGGGATCGGCACATCGAAGCAATCTTCTTGAAG 480  
Db 418 GACGGGTGGGCTCTCTCTGCGCGGGGATCGGCACATCGAAGCAATCTTCTTGAAG 477  
Qy 481 TGGCATGTGACCGGGGCTGTTGAGAGTCTGTCGCGAGTCTCTCTCTGCTGATCGGC 540  
Db 478 TGGCATGTGACCGGGGCTGTTGAGAGTCTGTCGCGAGTCTCTCTCTGCTGATCGGC 537  
Qy 541 TGCTGTCTTTGTCCTACT 600  
Db 538 TGCTGTCTTTGTCCTACT 597  
Qy 601 TTAGAAGCCATCTACTTTGTTATAGTACTCTCACTCTGTTAGGCTTTTGGCGATTATGTA 660  
Db 598 CTGAGAGCCATCTACTTTGTTATAGTACTCTCACTCTGTTAGGCTTTTGGCGATTATG 657  
Qy 661 CCCGGGATGCGACCGGGGCTGTTGAGAGTCTGTCGCGAGTCTCTCTCTGCTGATCGGC 720  
Db 658 GCGGGGCGGACCGGGGCTGTTGAGAGTCTGTCGCGAGTCTCTCTCTGCTGATCGGC 717  
Qy 721 TTGTTTGGCTAGCTTCT 780  
Db 718 CTGCTCGGCTGGCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 777  
Qy 781 GTGTCGCGGAACTCTGCGGAGAGTGGTGGGCTTAAAGGCTGTCAGGCTGCTAGCTGAGC 840  
Db 778 GTGTCGCGGAACTCTGCGGAGAGTGGTGGGCTTAAAGGCTGTCAGGCTGCTAGCTGAGC 837  
Qy 841 GGCACAGTACAGCGCGAGTACCCAGCAACTGGGCGGCTGAGCGGCTGAGCGGCTGAGC 900  
Db 838 GGCACAGTACAGCGCGAGTACCCAGCAACTGGGCGGCTGAGCGGCTGAGCGGCTGAGC 897  
Qy 901 GAGCAACCACTCTGCGGCT 960  
Db 898 GAGCAACCACTCTGCGGCT 945  
Qy 961 AGGCGGCTGCGGCT 1020  
Db 946 AGGCGGCTGCGGCT 1005  
Qy 1021 GCTCTGAGTATCCAGTACAGTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080  
Db 1006 GCGCTGAGTATCCAGCGAGAACCTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1065  
Qy 1081 GAGCGTGGTGGCTGCGGCT 1140  
Db 1066 GAGCGGCTGCGGCT 1125  
Qy 1141 AAGCCCTTCAGACCCCGGGTCTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1194  
Db 1126 AAGCCCTTCAGACCCCGGGTCTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1179

RESULT 2  
US-09-432-470-3  
; Sequence 3, Application US/09432470  
; Patent No. 6426197  
; GENERAL INFORMATION:  
; APPLICANT: David Malcolm Duckworth  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30190  
; CURRENT APPLICATION NUMBER: US/09/432,470  
; EARLIER FILING DATE: 1999-11-03  
; EARLIER APPLICATION NUMBER: UK 9923668.9  
; EARLIER FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: UK 9824048.4  
; EARLIER FILING DATE: 1998-11-03

; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 1218  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-432-470-3  
Query Match 68.2%; Score 814.4; DB 4; Length 1218;  
Best Local Similarity 81.5%; Pred. No. 8e-219;  
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;  
Qy 1 ATGCGCAGCACCACT 60  
Db 37 ATGCGCAGCACCACT 96  
Qy 61 GCTCTAGTGTTCAGGCT 120  
Db 97 GCGCTGGTGTTCGGGCT 156  
Qy 121 CATGCCCGAGACCACT 180  
Db 157 GAGTCTCCGAGAGAGTCT 216  
Qy 181 TTATCAAGCT 240  
Db 217 CTATCAAGAGAGTGGCTGATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276  
Qy 241 AATACAGCAACCACT 300  
Db 277 AGCAACAGAGCCAC---TCAGCTCTGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 333  
Qy 301 ATCATCACTACCATCGGCTATGGCAATATAGTCTTTACACAGATGCGCGGCTCTCTCT 360  
Db 334 ATCATCACTACCATCGGCTATGGCAATATAGTCTTTACACAGATGCGCGGCTCTCTCT 393  
Qy 361 TGTATCTTCTATGACTGTTGGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Db 394 TGCATCTTTTATGCGCTGTTGGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 453  
Qy 421 GACCGGCTGGGCT 480  
Db 454 GACCGGCTGGGCT 513  
Qy 481 TGCATATGTCACCGGGCTGTTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
Db 514 TGCACATGTCACCGGAGCTAGTAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 573  
Qy 541 TGCCTCTCTTTTCT 600  
Db 574 TGCCTCTCTTTTCT 633  
Qy 601 TTAGAAGCCATCTACTTTTATAGTACTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 660  
Db 634 CTGAGGCTCTACTTTTATAGTACTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 693  
Qy 661 CCCGGGATGCGACCGGGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
Db 694 GCGCGGCGGACCCCGGAGGACT 753  
Qy 721 TTGTTTGGCTCTAGCTTCT 780  
Db 754 CTGCTCGGCTCTAGCTTCT 813  
Qy 781 GTGTCCCGGAACT 840  
Db 814 GTGTCCCGGCACT 873  
Qy 841 GGCACAGTACAGCGGAGTACCCAGCAACTGGGCGGCTCTCTCTCTCTCTCTCTCTCTCT 900  
Db 874 GGCACAGTACAGCGGCGTACCCAGCAACTGGGCGGCTCTCTCTCTCTCTCTCTCTCTCT 933  
Qy 901 GAGCAACCACT 960





Db 847 AATCAAGTTAGTCAC-----TGGGACCTCGAAGCTCTTCTTCTTTGCTGGTACT 897  
Qy 301 ATCATCACTACCTCGGCTATGGCAATATAGTCTTACACACAGATGCGCGGCGCTCTCTTT 360  
Db 898 GTTATCAACACCATAGGATTTGAAACATCTCCCCAGAACTGAAGTGGAAAAATATTC 957  
Qy 361 TGTATCTTCTATGCACTGGTGGGGATCCCACTGTTGGGATGCTGCTGGCGGAGTCGGG 420  
Db 958 TGCATCATCTATGCTTGTGCGGAATTCCTCTCTTTGGCTTTCTACTGGCTGGGGTGGT 1017  
Qy 421 GACCGGCTGGGCTCTCTCTGCGCGGGGATCGGCCACATCGAAGCAATCTTCTTGAAG 480  
Db 1018 GATCAGCTAGAACTATATTGGAAGAAGAAATTGCCAAAGTGAAGACACATTTATTAAG 1077  
Qy 481 TGGCATGTGCGACCGGGCTGGTGAAGTCTGTCCGAGTGTCTTCTGCTGATCGGC 540  
Db 1078 TGGAAATGTTAGTCAGACGAAGATTCGTATCATCTCCACCATCATCTTCATCTCTTTGGC 1137  
Qy 541 TGGCTGCTTTGCTCTCACTCTCTACCTGCTGTTCTCTCTACATGAGAGCTGGAGCAAG 600  
Db 1138 TGTGTCTCTTTGCTCTCTCTGCTGCTCTCTCTGCTGCTATATTCAAGCACATAGAAGGCTGGAGCGC 1197  
Qy 601 TTAGAAGCCATCTACTTTGTTATAGTACTCTCACCCTCTAGGCTTTGSCGATTATGTA 660  
Db 1198 CTGAGAGCTATCTATTTTGGTTATCTCTGAGACCAATTTGATTTGGAGACTAGTG 1257  
Qy 661 CCGGGGATGGCCCGGGCGAAGAACTCTCCAGCCTACCGCGCTGGTGTGTTCTGGATC 720  
Db 1258 GCAGGTGGATCAGACATTAATCTCGGACTCTACAGCCTGTGGTGTGTTCTGGATC 1317  
Qy 721 TTGTTTGGCTAGCTACTTTCGCTCTGCTCTCACCACATCGGCAACTGGTGGCAGCA 780  
Db 1318 CTCGTTGGGCTGCTCTACTTTGAGCTGTTCTGAGCATGATTTGGGAGCTGGCTACCGGTG 1377  
Qy 781 GTCTCCGCGCACTCGGCGAGAGTGGTGGCTTAACGCGCAGAGCTGCTAGCTGACC 840  
Db 1378 ATCTTAAGAGAGAGAGAGAGTGGAGAGTTTCAAGCGCATGCCGCTGAGTGACA 1437  
Qy 841 GGCACAGTGACAGC 854  
Db 1438 GCCAATGTCAAGGC 1451

## RESULT 6

US-09-236-080-1  
; Sequence 1, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1246  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-236-080-1

Query Match 18.5%; Score 220.8; DB 3; Length 1246;  
Best Local Similarity 55.4%; Pred. No. 4e-52;  
Matches 454; Conservative 0; Mismatches 357; Indels 9; Gaps 1;

Qy 35 TGTGCTGCTTACTTGATATCTGGGGCTCTAGTGTCCAGGCTCTGGAGCAGCCTCAGC 94  
Db 166 TGGTTGCTCTATCTATCTATCATCGGAGCCACCGTGTTCAAAGCATTTGGAGCAGCCTCATG 225  
Qy 95 AGCAGCAGGCTCAGAGAAATGATCATGCGCGAGACCAAGTTTCTGAGGAGCATCCCT 154  
Db 226 AGATTTACAGAGGACACCAATTTGTATCCAGAGCAACATTCATATCCCAACATTCCT 285

Qy 155 GTGTGAGCCAGAAAGAGCCTGGAGGATTTTCAATCAAGCTCTCTGTTGAAGCCCTGGGAGGGG 214  
Db 286 GTGTCAATTCGACGGAGCTGGATGAACCTCATTCAGCAAAATAGTGGCAGCAATAAATGACAG 345  
Qy 215 GCGCAAAACCCAGAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTTGGAACCTGG 274  
Db 346 GGAATATACCGTTAGGAAACACCTCCAATCAATCAAGTCAC-----TGGGATTTGG 396  
Qy 275 GAGCGCCCTCTCTTTTCTCGGGACCATCATCACTACCATCGGCTATGGCAATATAGTCT 334  
Db 397 GAAGTTCTCTCTTTTCTGCTGGCACTGTTATTACACCATAGGATTTGGAACATCTCAC 456  
Qy 335 TACACACAGATGCGCGGCTCTCTTTTGTATCTTTATGACATGCTGGTGGGATCCCACTGT 394  
Db 457 CACGCACAGAGCGCGCAAAATATCTGTATCATCTATGCTTACTTGGGAATTTCCCTCT 516  
Qy 395 TCGGATGCTGCTGGCGGAGTCGGGACCGGCTGGGCTGCTCTCTGCGCGGGGATCG 454  
Db 517 TTGGTTTCTCTTGGCTGGAGTTGGAGATCAGCTAGGCACCATATTGGAAGAAAGAAATTG 576  
Qy 455 GCCACATCGAAGCAATCTTTGAAGTGGCATGTGCCACCGGGCTGGTGAGAAGTCTGT 514  
Db 577 CAAAGTGGAGATAGCTTTATTAACTGGAATGTTAGTCAGACCAAGATTCGCATCATCT 636  
Qy 515 CCGAGTGTCTCTCTGCTGATGGGCTGCTCTTTGTCTCTCACTCTTACCTTCTGCTGT 574  
Db 637 CAACATCATATTTATCTATTTTGGCTGTGATCTCTTTGGCTCTGCTCGCATCATAT 696  
Qy 575 TCTCTACATGAGAGCTGGAGCAAGTTAGAACCACTACTACTTTGTATAGTACTCTCA 634  
Db 697 TCAACACATAGAAGCTGGAGTGGCCCTGGAGCCCAATTTATTTTGGTTATCACTTAA 756  
Qy 635 CCACTGTAGGCTTTGGCGATTTATGTACCGCGGATGGCAGCGGAGAACTCTCCAGCCT 694  
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Qy 695 ACAGCCGCTGCTGCTGCTGATCTGATCTTTTGGCTTACCTTACTTCTGCTCTAGTCTCA 754  
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Qy 755 CCACCATCGCACTGGTTCGAGCAGTGTCCCGCGAATCTCGGCGAGAGTGGTGGCC 814  
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Qy 815 TAAAGGCACAGCTGCTAGCTGCGCGGACAGTGCAGTGACAGC 854  
Db 937 TCAGACACACGCTGCTGATGGACAGCCACGTCACAGC 976

## RESULT 7

US-09-336-643A-82  
; Sequence 82, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82

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; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1285)
US-09-336-643A-82

Query Match      18.5%; Score 220.8; DB 3; Length 3300;
Best Local Similarity 55.4%; Pred. No. 6.4e-52; Indels 9; Gaps 1;
Matches 454; Conservative 0; Mismatches 357;

QY 35 TGGTGTCTTACTTGGTATCTGGGCTCTAGTGTTCAGGCTCTGGAGCAGCTCAG 94
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 207 TGGTGTCTTACTTGGTATCTGGGCTCTAGTGTTCAGGCTCTGGAGCAGCTCAG 266
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 95 AGCAGCAGGCTCAGAGAAATGGATCATGCCGAGACAGTTTCTGAGGACCATCCCT 154
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 267 AGATTTCACAGAGACCACTTGTGATCCAGAAGCAACATTCATATCCCAATTCCT 326
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 155 GTGTGAGCCAGAGAGCTGGAGATTCATCAAGCTCTGTTGAAGCCTCTGGAGGGG 214
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 327 GTGTCAATTCGACGAGCTGATGACTCATTCAGCAATATGCGCAATTAATGAG 386
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 215 GCGCAAAACCCAGAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGAACCTGG 274
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 387 GGATTATACCGTTAGGAAACACCTCCCAATCAATCACTGCTAC-----TGGGATTTGG 437
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 275 GCAGGCGCTTCTTTCTCGGGAGCAATCATCACTACCATCGGTATGGCAATATAGTCT 334
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 438 GAAGTTCCTTCTTCTTGGCTGCTGTTTATTAACCACTAGGATTTGGAAACATCTCAC 497
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 335 TACACACAGATGCGGGGCTCTCTTTTGTATCTTCTATGCTGCTGGGATCCCACTGT 394
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 498 CACGACAGAGAGCGGCAAAATATCTGTATCATCTATGCTTACTTGGATTTCCCTCT 557
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 395 TCGGGATGCTCTCTCGCGGAGTCGGGACCGGCTGGGCTCTCTCTCTCGCGGGGATCG 454
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 558 TTGGTTTCTCTTGGCTGGAGTTGGAGATCAGCTAGGACCACTATTTGGAAAGGAATTG 617
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 455 GCGACATCGAAGCAATCTTTTGAAGTGGATGTCACCGGGCTGGTGAAGTCTGT 514
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 618 CCAAGTGGAAGATACGTTTATTAAGTGAATGTTAGTCAGCAACCAATTCGCAATCT 677
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 515 CCGCAGTCTCTCTCTGCTGATCGGCTGCTCTTGTCTCTCACTCTCACTTCTGTGT 574
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 678 CAACATCATATTTATCTATTTGGCTGTACTCTTTTGGCTCTGCTTGGCATCATAT 737
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 575 TCTCCTACATGGAGCTGGAGCAAGTTAGAACCATCTACTTTGTATAGTACTCTCA 634
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 738 TCAACACATAGAAGCTGGAGTGCCTTGGACGCCAATTTATTTTGTGTTATCACTTAA 797
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 635 CCACGTAGGCTTTGGCAATTTATACCGGCGATGGCAGCGGCAACTCTCCAGCT 694
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 798 CAATTTGGATTTGGTCACTACGTTGAGTGGATCCGATTTGAATATCTGACTTCT 857
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 695 ACCAGCGCTGTGTGTGTTCTGGATCTTTTGGCTAGCCCTACTTCCCTCAGTGTCTCA 754
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 858 ATAGCCTGTGTGTGTTCTGGATCTTCTGGATCTTCTTGGCTTGTCTTCTGCTCTGA 917
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 755 CCACATCGGCACATGTTGGAGCAGTGTCCCGCGAATCTCGGCGCAGAGATGGTGCC 814
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 918 GCATGTTGGAGTTGGCTCCGAGTGTATCTTAAAGACAAAGAGAGTGGGAGAT 977
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 815 TAACGGCACAGCTAGCTAGCGGCGCAGAGTACAGC 854
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 978 TCAGAGCACACCTGCTGAGTGGACCAACGTCACAGC 1017
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 8  
US-09-561-763-6  
; Sequence 6, Application US/09561763  
; Patent No. 6664373

```
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J. et al.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP2  
; CURRENT APPLICATION NUMBER: US/09/561,763  
; PRIOR FILING DATE: 2000-04-29  
; PRIOR APPLICATION NUMBER: 09/431,367  
; PRIOR FILING DATE: 01-11-1999  
; PRIOR APPLICATION NUMBER: US 09/259,951  
; PRIOR FILING DATE: 01-03-1999  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(996)  
; US-09-561-763-6  
  
Query Match      10.4%; Score 124.4; DB 4; Length 996;  
Best Local Similarity 54.5%; Pred. No. 4.3e-25;  
Matches 301; Conservative 0; Mismatches 236; Indels 15; Gaps 2;  
  
QY 226 GAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGGAACTGGGACGCGCTTC 285  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 262 GGAGCCAGCCTCTCTCAGCAACCAACCACTGGGCGCTGGGAGCTCGTGGGCTCTTC 321  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 286 TTTTCTCGGGACCAATCATCACTACCTGCTATGGCAATATAGTTTACACACAGAT 345  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 322 TTCTTTCTGTGTCCACCACTACCACTATGGCTATGGCACTGAGCCCCACAGGATG 381  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 346 GCGGGCGCTCTCTTTTGTATCTTATGCACTGGTGGGATCCCACTGTTGGGATGCTG 405  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 382 GCTGCCCGCTCTCTTGCACTCTTTTGGCTTGTGGGATCCCACTCAACCTCGTGTG 441  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 406 CTGGCGGAGTGGGGACCGGCTGGGCTCTCTCTGGCGGGGATCGGCCACATCGAA 465  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 442 CT-----CAACCGACTGGGGCACTCATGTCAGCAGGGAGTAAACCACTGGGCC 489  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 466 GCAATCTTCTGAAGTGGCATGTGCCACCGGGCTGGTGAAGAGTCTGTCCGAGTGTCT 525  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 490 AGCAGCTGGGGGACCTGGCAGGATCTGACAGCGCGGTGGCTGGCGGCTCTGGC 549  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 526 TTCTCTGATCGGCTGCTCTTTTGTCTCTTGTCTCACTCTACCTTCTGTCTCTACATG 595  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 550 GCGCTCTCTCGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 609  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 586 GAGAGCTGGAGCAAGTTAGAGCCATCTACTTTTGTATAGTACTCTCACCCTGTAGGC 645  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 610 GAGGCTGGAGCTACACAGAGGCTTCTACTTCCGCTTCTATCACCCTCAGCACCCTGG 669  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 646 TTTGGCGATTATGTACCCCGGATGGCAGCGGAGCA---ACTCTCAGCTTACAGCGG 702  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 670 TTGGCGACTACTGTATGGATGAACCCCTCCACAGAGGTACCACTGTGTGTACAGAAC 729  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 703 CTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 762  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 730 ATGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 789  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 763 GGCAACTGGTGTG 774  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 790 CTCTCCAGCTG 801  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
  
RESULT 9  
US-09-431-367B-6  
; Sequence 6, Application US/09431367B  
; Patent No. 6670149  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
```



RESULT 10  
US-09-561-763-4  
; Sequence 4, Application US/09561763  
; Patent No. 6664373  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Roy A. J. et al.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP2  
; CURRENT APPLICATION NUMBER: US/09/561,763  
; CURRENT FILING DATE: 2000-04-29  
; PRIOR APPLICATION NUMBER: 09/431,367  
; PRIOR FILING DATE: 01-11-1999

LENGTH: 1575  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (122)..(1117)  
US-09-431-367B-4

Query Match 10.4%; Score 124.4; DB 4; Length 1575;  
Best Local Similarity 54.5%; Pred. No. 5.3e-25;  
Matches 301; Conservative 0; Mismatches 236; Indels 15; Gaps 2;

QY 226 GAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGGAACTGGGCGGCTTC 285  
DB 383 GGAGCCAGCTCTCTCAGCAACACACAGCATGGGCGGCTGGGAGCTCGTGGCTCTTC 442  
QY 286 TTTTCTCGGGGACCATCATCACTTACCATCGGCTATGGCAATATAGTTTACACACAGAT 345  
DB 443 TTCTTTCTGTGTCACCATCATCAACCATTTGGCTATGGCAACCTGAGCCCCAACACGATG 502  
QY 346 GCCGGGCGTCTCTTTTCTATCTATGCACTGGTGGGATCCCACTGTTCGGGATGCTG 405  
DB 503 GCTGCCGCTCTCTGCACTCTTTTGGCTTTGGGGATCCCACTCAACCTCGTGGTG 562  
QY 406 CTGGCGGAGTCGGGACCGGCTGGGCTCTCTCTGCGCGGGGCTCGGCCACATCGAA 465  
DB 563 CT-----CAACCGACTGGGCGATCTCATGACGAGGAGTAAACCACTGGGCC 610  
QY 466 GCAATCTTTGAAGTGGCATGTCCACCGGGGCTGGTGAAGTCTGTCCGAGTGCTC 525  
DB 611 AGCAGGCTGGGGGCACTGGCAGGATCTTGACAAGGCGGCTGGCTGGCGGCTCTGGC 670  
QY 526 TTCTGTGTGATCGGCTGCTCTTTGTCTCACTCTCACTTCTGTTCTCTCATATG 585  
DB 671 GCCCTCTCTCGGGCTCTCTGCTCTCTGCTGCTGCAACCGCTGCTCTCTCCCATG 730  
QY 586 GAGAGCTGGAGCAAGTTAGAGCCATCTACTTTCTTATAGTACTCTCACCCTGTAGGC 645  
DB 731 GAGGCTGGAGCTACAGAGGGCTTCTACTTCCCTTCATCACCCTCAGCAGCGTGGC 790  
QY 646 TTTGGCGATTATGACCGCGGATGGCACCGGGGAGA---ACTTCCAGCTTACCAGCG 702  
DB 791 TTGGCGGACTAGTGATGGAATGAACCCCTCCAGAGGTACCACCTGTGTGACAGAAC 850  
QY 703 CTGGTGTGGTCTGGATCTTTGGCTAGCCTACTTTCGCTCAGTGTCTCACCACCATC 762  
DB 851 ATGTTGTCCTGTGGATCTCTTTGGGATGGATGGCTGGCTTGTATCACTCACTCATC 910  
QY 763 GGCAACTGGTTG 774  
DB 911 CTCCTCCAGCTG 922

RESULT 12  
US-09-561-763-3  
Sequence 3, Application US/09561763  
Patent No. 6664373  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A.J. et al.  
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
FILE REFERENCE: MNI-074CP2  
CURRENT APPLICATION NUMBER: US/09/561,763  
CURRENT FILING DATE: 2000-04-29  
PRIOR APPLICATION NUMBER: 09/431,367  
PRIOR FILING DATE: 01-11-1999  
PRIOR APPLICATION NUMBER: US 09/259,951  
PRIOR FILING DATE: 01-03-1999  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1497  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1497)  
US-09-561-763-3

Query Match 9.8%; Score 117.2; DB 4; Length 1497;  
Best Local Similarity 51.8%; Pred. No. 5.5e-23;  
Matches 384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;

QY 44 TTTTACTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCTTCAGCAGCAGG 103  
DB 41 TCTACTTGGCCATCGGGCGGCGATCTTCGAGTGTCTGGAGGACCCACACTGGAAGGAG 100  
QY 104 CTCAGAGAAAATGGATCATGGCCGAGACCAATTTCTGAGGGACCAATCCCTGTGTGAGCC 163  
DB 101 CCAAGAAAATCTACTACACACAGAACTGCTCTCAAGGAGTTCCTCGTCCCTGGGTC 160  
QY 164 AGAGAGCTGGAGGATTTTCAAGCTCTGGTGTGAGCCCTGGGAGGGGGCCAAACC 223  
DB 161 AGGAGGGCTGGACAAAGATCCTAGAGGTGTATCTGATGCTGACAGGACAGGGTGTGCCA 220  
QY 224 CAGAAACCACTGGACCAATAGCAGCAACCACTCATCAGCTTGGAACTGGGCGAGCGCT 283  
DB 221 TCAGAGGAAACAGACCTTCAACAC-----TGGAACTGGGCCAATGCA 265  
QY 284 TCTTTTCTCGGGGACCATCATCACTACCATCGGCTATGGCAATATAGTTTACACACAG 343  
DB 266 TGAATTTTGCAGCGACCGCTCATTTACCACTTGGATATGGCAATGTGGCTCCCAAGACC 325  
QY 344 ATGCCGGGCTCTCTTTTGTATCTTATGCACTGTGGGATCCCACTGTTCGGGATGC 403  
DB 326 CCGCGGCTGGCTCTCTTGTGTCTTCTGAGTCTCTTCGGGGTGGCTCTGC----- 378  
QY 404 TCCTGGCGGAGTCGGGACCGGCTGGGCTCTCTCTCTCGCGGGGCAATCGGCCACATCG 463  
DB 379 --CTGACGTGGATCAGTGCCTTGGGCAAGTTCTTCGGGGGACGTGCCAAGAGAC---TAG 433  
QY 464 AAGCAATCTTTTGAAGTGGCATGTGCCACCGGGCTGTGAGAGTCTGTCCGAGTGC 523  
DB 434 GGCAGTTCTTACCAAGAGAGGTGTGAGTCTGCGGAAGCGCAGATCAGTGCACAGTCA 493  
QY 524 TCTTCTGCTGATCGGCTGCTCTTGTCTCTCACTCTCACTTCTGTTTCTCTCTACA 583  
DB 494 TCTTCACTGTGGGGGCTCTAGTCCACCTGGTATCCACCCCTTCGTATTTCATGTGA 553  
QY 584 TGGAGAGCTGGAGCAAGTTAGAACCACTACTTTGTATAGTACTCTCACCCTGTAG 643  
DB 554 CTGAGGGTGGAACTACATCGAGGGCTCTACTCTCTTCTATCACCATCTCCCACTCG 613  
QY 644 GCTTGGCGATTTATGTACCGGGGATGGCACCGGCGAGAACTCTCCAGCC---TACCAGC 700  
DB 614 GCTTCGGTGACTTTGTGGCGGCTGTGAACCCAGCGCCAACTACCACGCCCTGTACCGCT 673  
QY 701 CGCTGGTGTGTTCTGGATCTTGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 760  
DB 674 ACTTCGTGGAGCTCTGGAICTACTTGGGGCTGGCTGGCTGGCTGGCTGGCTGGCT 733  
QY 761 TCGGCAACTGGTTGCGAGCAGT 782  
DB 734 AGGTGAGCATGTTTGTGGAAGT 755

RESULT 13  
US-09-431-367B-3  
Sequence 3, Application US/09431367B  
Patent No. 6670149  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A.J.  
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
FILE REFERENCE: MNI-074CP  
CURRENT APPLICATION NUMBER: US/09/431,367B  
CURRENT FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: 09/259,951

; PRIOR FILING DATE: 1999-03-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1497)  
US-09-431-367B-3

Query Match 9.8%; Score 117.2; DB 4; Length 1497;  
Best Local Similarity 51.8%; Pred. No. 5.5e-23;  
Matches 384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;  
QY 44 TTTACTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCTCAGAGCAGCAGG 103  
DB |||||  
41 TCTACTGGCCATCGGGGGCGGCGATCTTGAAGTGTGGAGGAGCCACACTGGAAGGAGG 100  
QY 104 CTCAGAGAAATGGATCATGGCCGAGACCAAGTTTCTGAGGGACCATCTCTGTGTGAGCC 163  
DB |||||  
101 CCAAGAAAAAATACTACACACAAGCTGCATCTGCTCAAGGAGTTCCCGTGCCTGGGTC 160  
QY 164 AGAAGAGCTGGAGGATTTTCATCAAGCTCTGTGTTGAAGCCCTGGAGGGGGGCGAAACC 223  
DB |||||  
161 AGAGGGCCCTGGACAAGATCTTAGAGTGTGTATCTGATGTCGAGGACAGGGGTGTGGCCA 220  
QY 224 CAGAAACCACTGACCAATAGCAGCAACCACTCATCAGCTTGGAACTGGGCGAGCGCT 283  
DB |||||  
221 TCACAGGAAACAGACTTCAACAC-----TGAACCTGGCCCATGCA 265  
QY 284 TCTTTTCTCGGGACCATCATCACTACCATCGGCTATGGCAATATAGTCTTACACACAG 343  
DB |||||  
266 TGATTTTTCAGGACCGTCATTACCAACCATTTGATATGCAATGCAATGGCTCCCAAGACC 325  
QY 344 ATGCCGGGCTCTCTTTTGTATCTTATGCACTGTGTGGGATCCCACTGTTCGGGATGC 403  
DB |||||  
326 CGCGGGTGGCTCTCTGTGTCTTATGTGTCTCTTCGGGGTGGCGCTCTGC----- 378  
QY 404 TGTGCGGGAGTCGGGGACCGGCTGGGCTCTCTCTGCGCGGGGCATCGGCCACATCG 463  
DB |||||  
379 --CTGACGTGGATCAGTGCCCTGGCAAGTTCTTCGGGGACGTGCCAAGAGAC---TAG 433  
QY 464 AAGCAATCTTTTGAAGTGGATGTCACCGGGCTGGTGAAGTCTGTCCGCAATGC 523  
DB |||||  
434 GGCAGTTCTTACCAAGAGAGGTGTGAGTCTGCGGAAGGCGCAGATCAGTGCACAGTCA 493  
QY 524 TCTTCTGTGATCGGCTGCTCTTTGTCTCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCT 583  
DB |||||  
494 TCTTCACTGTGTGGGGCTCTAGTCCACCTGTGTATCCACCTTCGTATTCATGTTGA 553  
QY 584 TGGAGAGCTGGAGCAAGTTAGAGCCATCTACTTTGTATAGTACTCTACCACTGTAG 643  
DB |||||  
554 CTGAGGGGTGGAATCACTAGAGGGCTCTACTACTCTCTCTCTCTCTCTCTCTCTCTCT 613  
QY 644 GCTTTGGCGATATGTACCGGGGATGGCAACCGGGGAGAACTCTCCAGGC---TACCAGC 700  
DB |||||  
614 GCTTCGGTGAATTTGTGGCGGGTGTGAACCCAGCGCCAACTACCAAGCCCTGTACCGCT 673  
QY 701 CGCTGT 760  
DB |||||  
674 ACTTCGTGAGCTCTGATCTACTTGGGGTGGCGCTGTCCCTTTTGTCAACTGGA 733  
QY 761 TCGGCACTGTTGCGAGCAGT 782  
DB |||||  
734 AGTGAGCATGTTTGTGGAAGT 755

RESULT 14

US-09-561-763-1

; Sequence 1, Application US/09561763

; Patent No. 6664373

; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J. et al.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP2  
; CURRENT APPLICATION NUMBER: US/09/561,763  
; CURRENT FILING DATE: 2000-04-29  
; PRIOR APPLICATION NUMBER: 09/431,367  
; PRIOR FILING DATE: 01-11-1999  
; PRIOR APPLICATION NUMBER: US 09/259,951  
; PRIOR FILING DATE: 01-03-1999  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3452  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(1506)  
US-09-561-763-1

Query Match 9.8%; Score 117.2; DB 4; Length 3452;  
Best Local Similarity 51.8%; Pred. No. 8.1e-23;  
Matches 384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;  
QY 44 TTTACTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCTCAGAGCAGCAGG 103  
DB |||||  
50 TCTACTGGCCATCGGGGGCGGCGATCTTGAAGTGTCTGAAGTGTCTGAAGGAGG 109  
QY 104 CTCAGAGAAATGGATCATGGCCGAGACCAAGTTTCTGAGGGACCATCTCTGTGTGAGCC 163  
DB |||||  
110 CCAAGAAAAAATACTACACACAAGCTGCATCTGCTCAAGGAGTTCCCGTGCCTGGGTC 169  
QY 164 AGAAGAGCTCGAGGATTTTCATCAAGCTCTCGTTGAAGCCCTGGGAGGGGGCGCAAAACC 223  
DB |||||  
170 AGAGGGCTTGACAAGATCCTAGAGTGTGTATCTGATGCTGCAGGACAGGGGTGTGCCA 229  
QY 224 CAGAAACCACTGGACCAATAGCAGCAACCACTCATACGCTTGGAACTCTGGGCGAGCCCT 283  
DB |||||  
230 TCACAGGGAAACAGACCTTCAACAA-----TGAACCTGGCCCAATGCAA 274  
QY 284 TCTTTTCTCGGGGACCATCATCACTACCATCGGCTATGGCAATATAGTCTTACACAG 343  
DB |||||  
275 TGATTTTTCAGCAGCAGCGCTATTACCAATTTGGATATGGCAATGCTGCCAAGACC 334  
QY 344 ATGCCGGGCTCTCTTTTGTATCTTATGCACTGTGTGGGATCCCACTGTTCGGGATGC 403  
DB |||||  
335 CGCGGGTGGCTCTCTTGTGTCTTATGTTCTCTTCGGGGTGGCGCTCTGC----- 387  
QY 404 TGTGCGGGAGTCTGGGGACCGGCTGGGCTCTCTTCTGCGCGGGGCATCGGCCACATCG 463  
DB |||||  
388 --CTGACGTGGATCAGTGCCCTGGGCAAGTTCTTCGGGGGACGTGCCAAGAGAC---TAG 442  
QY 464 AAGCAATCTTCTGAAGTGGCATGTGCCACCGGGGCTGGTGAAGTCTGTCCGAGTGC 523  
DB |||||  
443 GGCAGTTCTTACCAAGAGAGGTGTGAGTCTCGGAAGGCGCAGATCAGTGCACAGTCA 502  
QY 524 TCTTCTGTGATCGGCTGCTCTTGTCTCTCACTCTACCTCTCTGCTGCTGCTCTCTCTCA 583  
DB |||||  
503 TCTTCACTGTGTGGGGCTCTAGTCCACTGTGTATCCACCTTCGTTCGTATTCATGGTGA 562  
QY 584 TGGAGAGCTGGAGCAAGTTAGAAAGCCATCTACTTTGTATTATAGTACTCTCACCACTGTAG 643  
DB |||||  
563 CTGAGGGGTGGAATACATCGAGGGCTCTACTACTCTTCTTCTTCACTCACTCTCCACCATCG 622  
QY 644 GCTTTGGCGATTTATGATCCCGCGATGGCACCGGGCAGAACTCTCCAGCC---TACCAGC 700  
DB |||||  
623 GCTTCGGTGAATTTGTGGCGGTGTGAACCCAGCGCCAACTACCAAGCCCTGTATCCGCT 682  
QY 701 CGCTGT 760  
DB |||||  
683 ACTTCGTGAGCTCTGATCTACTTGGGGCTGGCGCTGTCCCTTTTGTTCACATGGA 742

QY 761 TCGGCAACTGGTTGCGAGCAGT 782  
Db 743 AGGTGAGCATGTTTGTGGAAGT 764

RESULT 15

US-09-431-367B-1  
; Sequence 1, Application US/09431367B  
; Patent No. 6670149  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP  
; CURRENT APPLICATION NUMBER: US/09/431,367B  
; CURRENT FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 09/259,951  
; PRIOR FILING DATE: 1999-03-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3452  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(1506)  
US-09-431-367B-1

Query Match 9.8%; Score 117.2; DB 4; Length 3452;  
Best Local Similarity 51.8%; Pred. No. 8.1e-23;  
Matches 384; Conservative 0; Mismatches 328; Indels 30; Gaps 4;  
QY 44 TTTACTTTGGTATCTGGGGCTCTAGTGTTCAGGCTCTGGAGCAGCCTCAGAGCAGCAGG 103  
Db 50 TCTACTTGGCCATCGGGGGCGCGGATCTTCGAGTGTCTGGAGGAGCCACACTGGAAGAGG 109  
QY 104 CTCAGAGAAATGGATCATGCGGACAGCAGTTTCTGAGGGACCATCCCTGTGTGAGCC 163  
Db 110 CCAAGAAACTACTACACAGAGAGCTGCTCTGCTCAAGGAGTTCCCGTGCCTGGGTC 169  
QY 164 AGAAGCCCTGGAGGATTTTCATCAGCTCTCTGTTGAGCCCTGGAGGGGGCGCAACC 223  
Db 170 AGAGGGCCCTGGACAGATCTTAGAGGTGTATCTGATGTGAGGACAGGGGTGGCCA 229  
QY 224 CAGAAACAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGAACTGGGCGAGCGCCT 283  
Db 230 TCACAGGGAACAGACCTTCAACAC-----TGGAACTGSCCAATGCAA 274  
QY 284 TCTTTTCTCGGGACCATCATCACTACCATCGGCTATGCAATATAGTCTTACACAG 343  
Db 275 TGATTTTTCAGCGACCGCTCATACCACTTGGATATGCAATGTGGCTCCCAAGACCC 334  
QY 344 ATGCCGGGCTCTTTTGTATCTTCTATGACTGGTGGGGATCCCACTGTTCCGGATGC 403  
Db 335 CCGCGGCTCGCTCTCTGTGTCTTCTATGTTCTTTCGGGGTGCCTCTGC----- 387  
QY 404 TGCTGGCGGAGTGGCGGACCGGCTCGCTCTCTCGCGGGGATCGGCCACATCG 463  
Db 388 --CTGACGTGATCAGTGGCCCTGGGCAAGTCTTCGGGGGACGTGCCAAGAGAC---TAG 442  
QY 464 AAGCAATCTTTTGAAGTGGCANTGCCACCGGGGCTGGTGAAGAGTCTGTCCGCAAGTGC 523  
Db 443 GGCAATTCCTTACCAAGAGAGGTGTGAGTCTCGGAAGGGCGCAGATCACGTGCACAGTCA 502  
QY 524 TCTTCCTGCTGATCGGCTGCTCTTGTCTCTCACTACCTACCTGCTGCTTCTCTACA 583  
Db 503 TCTTCATCGTGTGGGGGCTCTAGTCCACTGCTGATCCCACTTCCGATTTATGTTGA 562  
QY 584 TGGAGAGCTGGAGCAAGTTAGAAGCCATCTACTTTTGTATAGTACTCTCACCACCTAG 643  
Db 563 CTGAGGGGTGGAATACATCAGAGGGCTCTACTACTCTCTTCATCACCACCTCCACCATCG 622  
QY 644 GCTTTGGCGATTATGTATACCGGGCGATGGCACCGGGCGAGAACTCTCCAGCC---TACCAGC 700

Db 623 GCTTCGGTGACTTTGTGGCCGGTGTGAACCCCGAGCGCAACTACCAACGCTGTACCGCT 682  
QY 701 CGCTGGTGTGGTTCTGGATCTTGTGGCTAGCCTACTTGGCCTCAGTGTCTCACCACA 760  
Db 683 ACTTCGTGGAGCTCTGGATCTACTTGGGGCTGGCTGTCCCTTTTGTCAACTGGA 742  
QY 761 TCGGCAACTGGTTGCGAGCAGT 782  
Db 743 AGGTGAGCATGTTTGTGGAAGT 764

Search completed: February 2, 2005, 20:30:38  
Job time : 126 secs

Db 61 GCCTGGTGTTCGGGGCCCTGGAGCAGCCCGAGCAGCAGCCCGAGCGAGCTGGGG 120





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Db 676 CTGAGGCCATCTACTTTGTTCATAGTGACCTTACCACGCTGGCTTTGGCGACTATGTG 735
QY 661 CCGCGGATGGACCGGGCAGAACTCTCCAGCCTTACCAGCGCTGGTGTGTTCTGGATC 720
Db 736 GCGGCGCGGACCCAGGAGGACTCCCGCGCTATCAGCGCTGTGTGTTCTGGATC 795
QY 721 TTGTTTGGCTAGCTACTTTCGCTCAGTGTCTCACCACCATCGGCAACTGTTTGGAGCA 780
Db 796 CTGCTGGCTTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGCAACTGCTGCGAGTA 855
QY 781 GTGTCCCGCGAATCTGGGCGAGAGATGGGTGGCTTAAGGCACAGGCTGTACTGTGACC 840
Db 856 GTGTCCCGCGCACTCGGCGAGAGATGGCGGCTCTACGGCTCAGGCTGCGACTGTGACT 915
QY 841 GGCACAGTGAACGCGGAGTGACCCAGCGAACTGGGCGCCAGCGCCCGCGCCGAGAGAG 900
Db 916 GGCACAGTGAACGCGGCGTGACCCAGCGAGCGCGGCGCCCGCGCCCGCGGAGAG 975
QY 901 GAGCAACCACTCTGCGCTCTCTTTGCGGCGCACCGCTGTCTGTGTGAGCCAGCGCGC 960
Db 976 GAGCAGCCACTGC-----TGCTCCACCGCGCTGTCCAGCGAGCGCTGGGC 1023
QY 961 AGGCGCGCTCCCTGCACCGCGAGAGAGTTGAGACTCCGTCCCGCGCCAGCGCTCA 1020
Db 1024 AGGCGCGGATCCCTTTCGCGCCCGGAGAGGCTCAGCGGCTTCCCGCGCCAGCGCTCG 1083
QY 1021 GCTCTGATTAACCCAGTGAAGATCTGGCTTCTATCGACGAGTCTCAGACGCGAGGT 1080
Db 1084 GCGCTGATTAATCCACGAGAACTGGCTTCTATCGACGAGTCTCAGTACGAGAGC 1143
QY 1081 GAGCGTGGCTGTGCGCTTCCCTCGGCTCTCTCGGCTCGCGCGCGAGCCCAACCCATCAA 1140
Db 1144 GAGCGGCTGCGCGCTGCGCGCGCGCGCGAGAGTTCGCGCGCGCGCGCGCGCGAGG 1203
QY 1141 AAGCTTCCAGACCGCGGCTCTGGCGAGTCTCGGCGAGTCTCGGCGAGCGCGCTGGG 1194
Db 1204 AAGCGCGTGGCGCGCGCGCGCGCGCGCGCTCCCGAGACAAAGCGCGTGGCGGTG 1257

RESULT 4
US-10-345-680-45
; Sequence 45, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
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; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1260)
US-10-345-680-45
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Query Match      68.2%; Score 814.4; DB 15; Length 1260;
Best Local Similarity 81.5%; Pred. No. 1.2e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;
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QY 1 ATGCGCAGCACACACTCTCGCTCTGCTGGCACTGGTGTCTTTTACTTGTGTATCTGGG 60
Db 79 ATGCGCAGCACACACTCTCGCTCTGCTGGCACTGGTGTCTTTTACTTGTGTATCTGGT 138
QY 61 GCTCTAGTGTTCAGGCTCTGAGCAGCTCTCAGCAGCAGGCTCAGAGAAATGGAT 120
Db 139 GCGCTGTGTTCGCGGCTCTGAGCAGCTCTGAGCAGCAGGCTCAGAGGAGCTGGGG 198
QY 121 CATGCGCAGACCACTTTCTGAGGACCATCTCTGTGTGAGCCAGAGAGCTGGAGAT 180
Db 199 GAGGTCGAGAGAAAGTTCTGAGGCGCCATCCGTGTGTGAGCGACCCAGAGCTGGGCGCTC 258
QY 181 TTCATCAAGCTCTCTGTGTGAAGCCCTGGGAGGGGGCGCAACCCAGAAACCAAGCTGGACC 240
Db 259 CTCATCAAGAGGTGGCTGATGCCCTGGGAGGGGGTCCGACCCAGAAACCAAGCTGGACC 318
QY 241 AATAGCAGCAACCACTCATCAGCTTGGAACTCTGGGAGCGCTTCTTTTCTGCGGGAGC 300
Db 319 AGCAACAGCAGCGCAC---TCAGCTGGGACCTGGGCGAGCGCTTCTTTTCTCAGGGACC 375
QY 301 ATCATCACTACCATCGGCTATGCAATATAGTCTTACACAGATGCGCGGGCTCTCTTT 360
Db 376 ATCATCACCACCATCGGCTATGCAATATGCGCCCTGCGCACAGATGCCGGGCGCTCTTTC 435
QY 361 TGTATCTTCTATGCACTGCTGGGGATCCCACTGTTCGGGATGCTGCTGGCGGAGTCGGG 420
Db 436 TGCACTTCTATGCGCTGTGTGGGATTCGCTGTGTGGGATCTACTGCGAGGGTCTGGG 495
QY 421 GACCGCTGGGCTCTCTCTGCGCGGGGATGCGGCACATCGAAGCAATCTCTTTGAAG 480
Db 496 GACCGCTGGGCTCTCTCTGCGCCATGCGATCGGTTCACATTAAGCCATCTCTTTGAAG 555
QY 481 TGGCATGTGCCACCGGGGCTGTGAGAGTCTGTCCGAGTGTCTTCTGTGTGATCGGC 540
Db 556 TGGCAGTGTGCCACCGGAGCTAGTAAGAGTGTGTGCGCGATGCTTCTCTGTGTGATCGGC 615
QY 541 TGCTCTCTTTTGTCTCTACTCTCTACTCTTCTGTTTCTCTACATGAGAGCTGGAGCAAG 600
Db 616 TGCTCTCTTTTGTCTCTACTCTCTACTCTTCTGTTTCTCTATATGAGAGCTGGAGCAAG 675
QY 601 TTAGAAGCCATCTACTTTGTATAGTACTCTACCATCTGAGGCTTTGGCGATTAATGTA 660
Db 676 CTGGAGGCCATCTACTTTGTCTAGTACGCTTACCACTGAGGCTTTGGCGATATGTG 735
QY 661 CCGCGGATGGCAGCGGCGAGAACTCTCCAGCTTACCGCGCTGCTGTGTGTGTGTGTGATC 720
Db 736 GCGGCGCGGAGCCCGAGGAGACTCTCCCGGCTATCAGCGCTGTGTGTGTGTGTGTGATC 795
QY 721 TTGTTTGGCTTAGCTTACTTTCGCTCAGTGTCTCACCACTCGGCAACTGGTTTGGAGCA 780
Db 796 CTGCTCGGCTTGGCTTACTTTCGCTCAGTGTCTCACCACTCGGCAACTGGCTGCGAGTA 855
QY 781 GTGTCCCGCGCACTCGGCGAGAGATGGGTGGCTTAAGGCACAGGCTGTACTGTGACC 840
Db 856 GTGTCCCGCGCACTCGGCGAGAGATGGGCGGCTCAGCGCTCAGGCTGCGACTGTGACT 915
QY 841 GGCACAGTGAACGCGGAGTGACCCAGCGAACTGGGCGCCAGCGCCCGCGCGAGAGAG 900
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Db	1084	GCCCTGATTATCCACGGAGAACTGGCCCTTATCAGCAGTGCTCGGATACGCAGAGC	1143
Qy	1081	GAGCGTGGCTGTGCCCTCTGCTCTGGGGTCTCTCGGGTCCGCGCGAACCCACCCATCCAAA	1140
Db	1144	GAGCGGGCTGCCCGCTGCCCGCGCGCGAGAGGTGCGCGCGCCCAAAATCCCCCAGG	1203
Qy	1141	AAGCCTTCCAGACCCCGGGGTCTCTGGCGCATCCCGAGACAAAGCGCGTGC CGGTG	1194
Db	1204	AAGCCCTGTGGGCGCCCGCGGCCCGGGCGTCCCGAGACAAAGCGCTGCCGGT	1257

## RESULT 6

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US-09-828-035-1
; Sequence 1, Application US/09828035
; Patent No. US20020034781A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF
; FILE REFERENCE: MMI-142
; CURRENT APPLICATION NUMBER: US/09/828,035
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,734
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84) .. (1340)
US-09-828-035-1

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Qy 541 TGCGTCTCTTTGTCCTCACTCTCACTTCGTTGTTCTCTCACTGAGAGACTGGAGCAAG 600  
Db 699 TGCGTCTCTTTGTCCTCACTTCGTTGTTCTCTCACTGAGAGACTGGAGCAAG 758  
Qy 601 TTAGAGCCATCTACTTTTGTATAGTGACCTCTCAACCACTCTAGGCTTTGGCGATATATGTA 660  
Db 759 CTGAGGCCATCTACTTTTGTATAGTGACCTCTCAACCACTCTAGGCTTTGGCGATATATGTA 818  
Qy 661 CCGCGCGATGGCACCGGCGAGAACTCTCCAGCCTTACAGCGCTGTGTGGTTCTGGATC 720  
Db 819 GCCGGCGGACCCAGGCGAGGACTCCCGGCGCTATCAGCGCTGTGTGGTTCTGGATC 878  
Qy 721 TTGTTTGGCCCTAGCTACTTTCGCTCAGTCTCTCACCACATCGGCACTGGTTGCGGACGA 780  
Db 879 CTGCTCGGCTGTGCTTACTTTCGCTCAGTCTCTCACCACATCGGCACTGGTTGCGGACGA 938  
Qy 781 GTGTCCCGCGAACTCGGGCAGAGATGGGTGGCTTAACGGCACAGGCTGTAGCTGTGACCC 840  
Db 939 GTGTCCCGCGCACTCGGGCAGAGATGGGGCGGCTCAGGGCTCAGGCTGCCAGCTGGACT 998  
Qy 841 GGCACAGTGACAGCGGAGTGACCCAGCAAACTGGGGCCCAAGCGCCCGCGCCAGAGAA 900  
Db 999 GGCACAGTGACAGCGGCGGTGACCCAGCAGCGGGCGCGCCCGCGCGCGGAGAA 1058  
Qy 901 GAGCAACACTCTCGCCCTCTCTTTTCCGGCACCGCTCTGTGTTGAGCCAGCCCGCC 960  
Db 1059 GAGCAGCACTGC-----TGCTTCCACCGCCCTGTCCAGCGCAGCCGCTGGCC 1106  
Qy 961 AGGCGCGCTCCCTGTCACCCGAGAGAAAGTTGAGACTCCTGCTCCCGCCCAAGCGCTCA 1020  
Db 1107 AGGCGCGATCCCTTTCGCCCGCGAGAGGCTCAGCGCTTCCCGCCCAAGCGCTCG 1166  
Qy 1021 GCTCTGGAATACCCCACTGAGAACTTGGCTTATGACAGAGTCTCAGACACGACAGT 1080  
Db 1167 GCCCTGATTATCCAGCAGAACTGGCTTATGACAGAGTCTCCTCGGATACGACAGC 1226  
Qy 1081 GAGCGTGGCTGCGCTGCTCGGGCTCTCGGGGTGCGCGGACCAACCCATCCAAA 1140  
Db 1227 GAGCGGGCTGCGCGCTGCGCGCGCGCGAGAGGTGCGCGCGCCCAATCCCCCAGG 1286  
Qy 1141 AAGCCTTCCAGACCCCGGGTCTCTGGCGAGCTCCGAGACAAAGCGCTGCCGGTG 1194  
Db 1287 AAGCCGTGCGGCCCGCGCGCGCGCGCGTCCCGAGACAAAGCGCTGCCGGTG 1340

RESULT 7  
US-10-146-738-28  
; Sequence 783, Application US/10146733  
; Publication No. US20030165891A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Glucksmann, Maria A.  
; APPLICANT: Siles-Santiago, Inmaculada  
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
; TITLE OF INVENTION: NMNDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MNI-248  
; CURRENT APPLICATION NUMBER: US/10/146,733  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 60/185,938  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/515,520  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/518,866  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: US 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: US 60/195,993  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: US 60/199,799  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/233,537



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; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1343)
; US-10-352-684A-7

Query Match      68.2%; Score 814.4; DB 15; Length 1408;
Best Local Similarity 81.5%; Pred. No. 1.2e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

QY      1  ATGCGCAGCACCACTCTGCTGGCTCTGCTGGCACTGGTGCTGCTTTACTTTGGTATCTGGG 60
DB      162 ATGCGCAGCACCAAGCTCTGCTGGCCCTGCTGGCGCTGGTCTTGTCTTACTTGGTGTCTGGT 221

QY      61  GCTCTAGTGTTCAGGGCTCTGGAGCAGGCTCACGAGCAGCAGGCTCAGAGAAAAATGGAT 120
DB      222 GCCCTGGTGTTCGGGGCCCTGGAGCAGGCCACGAGCAGCAGGAGCCAGAGGGAGCTGGGG 281

QY      121 CATGGCCGAGACCAAGTTTCTCAGGGAACAATCCCTGTGTGAGCCAGAGAGAGCTGGAGAT 180
DB      282 GAGGTCCGAGAGAAGTTCTCTGAGGGCCCATCCGTGTGTGAGCGCACGAGGAGCTGGGCGTC 341

QY      181 TTCAATCAAGCTCTGGTTGAAGCCCTGGAGGGGGCGCAAAACCCAGAAACCAAGCTGGAGCC 240
DB      342 CTCAATCAAGAGGTGGCTGATGCCCCCTGGAGGGGGTGGGACCCGAGAACCAACTCGACC 401

QY      241 AATAGCAGCAACCACTCATCAGCTTGGAAACCTGGGCACGCGCTCTTTTCTCGGGGACC 300
DB      402 AGCAACACAGCCAC--TCAGCCTGGGACCTGGGCAGCGCTCTTTTCTCAGGGACC 458

QY      301 ATCATCACTACAATCGGCTATGGCAATATAGTCTTTACACACAGATGCCGGGGCTCTCTTT 360
DB      459 ATCATCAACCAATCGGCTATGGCAATATGGCCCTTCGCGCACAGATGCCGGGGCGCTCTTC 518

QY      361 TGTATCTTCTATGCACTGGTGGGATCCCACTGTTTCGGGATGCTGTCGGCGGAGTCTCGGG 420
DB      519 TGCATCTTTATGCGCTGGTGGGATTCGCGTGTGTTGGATCTTACTGCGAGGGTCTCGGG 578

QY      421 GACCGGCTGGGCTCCCTCTCTGCGCGGGGCATCGGCCAATCGAAGCAATCTTCTTGAAG 480
DB      579 GACCGGCTGGGCTCCCTCCCTGCGCCATCGCATCGGTCAATTTGAAGCCATCTTCTTGAAG 638

QY      481 TGGCATGTGCCACCGGGGCTGGTAGAAGTCTGTCCGAGTGTCTTCTGCTGATCGGC 540
DB      639 TGGCATGTGCCACCGGAGCTAGTAAGATGCTGTGCGCGATGCTTTCTGCTGATCGGC 698

QY      541 TGCCTGCTTTTGTCTCTCACTCTACTCTTCTGCTGTTCTCTCTACATGAGAGCTGGAGCAAG 600
DB      699 TGCCTGCTTTTGTCTCTCAAGCCAGTTCGTTCTGCTATATGAGAGCTGGAGCAAG 758

QY      601 TTAGAAGCCATCTACTTTGTTATGATGACTCTCACCACTGTAGGCTTTGGCGATATGTA 660

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; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1343)
US-10-391-399-18

Query Match      68.2%; Score 814.4; DB 15; Length 1408;
Best Local Similarity 81.5%; Pred. No. 1.2e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;

QY 1 ATGCGCAGACCACTCTCTGGCTCTGTGGCACTGGTGTCTTACTTGTATCTGGG 60
DB 162 ATGCGCAGACCACTCTCTGGCTCTGTGGCTCTGTGGCTCTGTGGCTCTGTGG 221
QY 61 GCTCTAGTGTTCAGGCTCTGGAGCAGCCTCAGCAGCAGCAGCAGCAGCAGCAG 120
DB 222 GCCTCTGTGTTCGGGCGCTTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 281
QY 121 CATGGCGCAGACCACTTCTTGAGGACCACTCTGTGTGAGCAGCAGCAGCAGGAT 180
DB 282 GAGGTCCGAGAGAGTTCCTGAGGCGCCATCCGTGTGTGAGCAGCAGGCTGGCCCTC 341
QY 181 TTCAATCAAGCTCTCTGTGAGCCCTTGGAGGGGGGCGCAAAACCAAGAACTGGACC 240
DB 342 CTATCAAGAGGAGTGTGATGCTGCTGGAGGGGGTGGCAGCCAGAACTCGACC 401
QY 241 AATAGCAGCAACCACTCATCAGCTTGGAACTGGGAGCGCTTCTTTCTCGGGACC 300
DB 402 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGAGCGCCCTCTTTTCTCAGGGAC 458
QY 301 ATCATCACTACCACTCGCTATGCAATATAGTCTTACACACAGATCGCGGGCTCTCTTT 360
DB 459 ATCATCAACCACTCGCTATGCAATATAGTCTTACACACAGATCGCGGGCGCTCTTC 518
QY 361 TGTATCTTCTATGACTGTGGGATCCCACTGTTCGGGATGCTGTGGGGAGTCTGGG 420
DB 519 TGCATCTTTATGCGTGTGGGATTCGCTGTGTTGGGATCTACTGGCAGGGGTCTGG 578
QY 421 GACCGCTGGCTCTCTCTGCGCGGGGATCGGCACATCGAAGCAATCTTCTTGAAG 480
DB 579 GACCGCTGGCTCTCTCTGCGCGGGGATCGGCACATCGGATCGGATCGGATCTTCTTGAAG 638
QY 481 TGGCATGTGCGCACCGGGCTGGTGAGAGTCTGTGCGCAGTCTTCTGCTGTATCGGC 540
DB 639 TGGCAGTGGCACCGAGCTAGTAAGAGTCTGTGCGGATGCTTCTGCTGTATCGGC 698
QY 541 TGCCTGCTTTGTCTCTCACTCTCTACTCTGTTTCTCTACATGAGAGCTGAGCAAG 600
DB 699 TGCCTGCTTTGTCTCTCACTCTCTACTCTGTTTCTCTACATGAGAGCTGAGCAAG 758
QY 601 TTAGAAGCCATCTACTTTGTATGACTCTCACCAGTGTAGCTTTGGCGATATGTA 660
DB 759 CTGGAGGCCATCTACTTTGTATGACTCTCACCAGTGTAGCTTTGGCGATATGTA 818
QY 661 CCCGGGATGGCACCGGCGAGAACTCTCCAGCCTTACCAGCGCTGTGTGTCTGATC 720
DB 819 GCCGGCGGACCCAGCAGGACTCTCCCGGCTATCAGCCGCTGTGTGTCTGATC 878
QY 721 TTGTTTGGCTAGCTACTTCTGCTCAGTGTCTACCAACATCGGCAACTGTGTCGAGCA 780
DB 879 CTGCTCGGCTGTGCTTACTTCTGCTCAGTGTCTACCAACATCGGCAACTGTGTCGAGTA 938
QY 781 GTCTCCGCGCAACTCTGGGAGAGATGGGTGGCTTAACGGCAGGCTGTACTGTGACC 840
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DB 939 GTGTCCCGCCACTCGGCGCAGAGATGGCGGCTCTCAGGCTCAGGCTCCAGCTGGACT 998
QY 841 GGCACAGTGCAGCGCGAGTGCACCCAGCGAACTGGGCCAGCCCGCCCGCCGAGAAAG 900
DB 999 GGCACAGTGCAGCGCGAGTGCACCCAGCGAGCGCGGCGCGCGCGCGCGCGGAGAAAG 1058
QY 901 GAGCAACCACTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
DB 1059 GAGCAGCCACTGC-----TGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 1106
QY 961 AGCGCCCGGCTCCCTGACCCGCGAGAGAGTGTGAGACTCCGTCCTCCCGCCAGCGCTCA 1020
DB 1107 AGCGCCCGGATCCCTTCCGCCCCCGAGAGGCTCAGCGGCTTCCCGCCCGCGGCTCG 1166
QY 1021 GCTCTGATTAACCCAGTGAAGATCTGGCTTTCATCGAGAGTCTCTCAGACGAGAGT 1080
DB 1167 GCCTTGGATTATCCAGCGAGAACTGGGCTTTCATCGAGAGTCTCTCGATACGAGAGC 1226
QY 1081 GAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1227 GAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
QY 1141 AAGCTTTCAGACCCCGGGTCTCTGGCGACTCCGAGACAAAGCCCTGCGGCTG 1194
DB 1287 AAGCCGCTGCGGCGCCCGGCGCTCCCGAGACAAAGGCTGCGGCTG 1340

RESULT 10
US-10-768-158-11
; Sequence 11, Application US/10768158
; Publication No. US20040204359A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Elisabeth, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012PIRNONIM
; CURRENT APPLICATION NUMBER: US/10/768,158
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2747
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)...(1310)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2747)
; OTHER INFORMATION: n = A,T,C or G
US-10-768-158-11

Query Match      68.2%; Score 814.4; DB 18; Length 2747;
Best Local Similarity 81.5%; Pred. No. 1.5e-233;
Matches 973; Conservative 0; Mismatches 206; Indels 15; Gaps 2;
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1 ATGGCAGCACCACACTCCTGGCTCTGTGGCACTGGTGCTTTACTTGTGTAATCTGGG 60  
Db  
129 ATGGCAGCACCACAGCTCTGGCCCTGTGTGGCGCTGGTCTTGTCTTACTTGGTGCTGGT 188  
Qy  
61 GCTCTAGTGTTCAGGCTCTGAGCAGCCTCACGAGCAGCAGGCTCAGAGAAATCGAT 120  
Db  
189 GCCCTGTGTTCGGGCGCTGGAGCAGCCCAAGCAGCAGGCGCCAGAGGAGCTGGG 248  
Qy  
121 CNTGGCCGACACAGTTTCTGAGGGACCACTCCTGTGTGAGCAGAAAGAGCCTGGAGAT 180  
Db  
249 GAGTCCGAGAGAGTTCTTGAGGGCCATCGTGTGTGAGCAGCAGGACTGGGCGCTC 308  
Qy  
181 TTCAATCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGCGAAACCCAGAAACAGCTGAGCC 240  
Db  
309 CTCATCAAGGAGTGGTGATGCTCTGGAGGGGGTGGCGAACCCAGAAACCAATCTGCACC 368  
Qy  
241 AATAGCAGCAACACTCATCAGCTTCGGAACCTGGGCAGCGCTCTTTTCTCCGGGAGCC 300  
Db  
369 AGCAACAGCAGCCAC---TCAGCGCTGGACCTGGGCAGCGCTCTTTTCTCAGGAGCC 425  
Qy  
301 ATCATCACTACCATCGGCTATGGCAATATAGTCTTACACAGATGCGGGGCTCTCTTT 360  
Db  
426 ATCAATCACCACTCGGCTATGGCAATGTGGCCCTCGGCACAGATGCGGGCGCTCTTTC 485  
Qy  
361 TGTATCTTCTATGACATCTGGTGGGATCCCACTGTTCCGGATGCTGTCGGGAGCTCGGG 420  
Db  
486 TGCATCTTTATGGCGCTGGTGGGATTCGCTGTTTGGGATCCTACTGGCAGGGTCTGG 545  
Qy  
421 GACCGGCTGGGCTCTCTCTGGCGGGGCGATCGGCCACATCGAAGCAATCTTTTGAAG 480  
Db  
546 GACCGGCTGGGCTCTCTCTGGCGGCCATGCGGATCGGTCAATTTGAAGCCATCTTCTTGAAG 605  
Qy  
481 TGGCATGTGCCACCGGGGCTGGTGAGAAATCTGTCCGAGTGTCTTCTGCTGATCGGC 540  
Db  
606 TGGCAGTGGCCACCGGAGCTAGTAAGAGTGTGTCCGCGATGCTTTCTGCTGATTCGGC 665  
Qy  
541 TGGCTGCTTTTGTCTTCTCACTTACCTTCTGTTCTTCTTACATGAGAGCTGGAGCAAG 600  
Db  
666 TGGCTGCTTTTGTCTTCTCACTTACCTTCTGTTCTTCTTATGAGGACTGGAGCAAG 725  
Qy  
601 TTAGAAGCCATCTACTTTTGTATATAGTGACTCTCAACATCTAGCTTTGGCGATTATGTA 660  
Db  
726 CTGGAGGCATCTACTTTGTATAGTGAAGCTTACCACCGCTGGGCTTTGGCGACTATGTG 785  
Qy  
661 CCGCGGATGGCAACCGGGAGAACTCTCAGCCTACAGCGCTGTGTGTTCTCGATC 720  
Db  
786 GCGGCGCGGACCCAGGAGGACTCCCCGGCCTATCAGCGCTGTGTGTTCTCGATC 845  
Qy  
721 TTGTTTGGCTTAGCCTTACTTTCGCTCAGTGTCTCAACCACTCGGCAACTGGTTGCGAGA 780  
Db  
846 CTGCTCGGCTTGCTTACTTTCGCTCAGTGTCTCAACCACTCGGCAACTGGTTGCGAGA 905  
Qy  
781 GTCTCCCGCGCACTCGGCGAGAGATGGGTGGCTTAACGGCAAGGCTGTAGCTGGACC 840  
Db  
906 GTGTCCCGCGCACTCGGCGAGAGATGGGTGGGCTTACGGCTCAGGCTGTGAGCTGGACT 965  
Qy  
841 GGCACTGTGACGCGGAGTGAACCGAGCACTGGGCGGAGCTGGCGCCCGCGCCGAGAGAG 900  
Db  
966 GGCACAGTGAACGCGGCGTGAACCCAGCAGCGCGGCGCCCGCGCCGCGGAGAG 1025  
Qy  
901 GAGCAACCACTCTCTGCGCTCTCTTTTGGCGGACCGCTGTGTTGTGAGCAGCGCGC 960  
Db  
1026 GAGCAGCACTGC-----TGCCTTCACCGCTCTGTCCAGCGCGCTGGGCTGGG 1073  
Qy  
961 AGGCCGGCTCTCCCTGACCCCGAGAGAGTGTGAGCTCCGTCCTCCCGCCCAAGGCTCTCA 1020  
Db  
1074 AGGCCCGATCTCCCTTTCGCGCCCGAGAGGCTCAGCGCGCTTTCCTCCCGCCCAAGGCTCTCG 1133  
Qy  
1021 GCTCTGATTTACCCCACTGAGAAATCTGGGCTTCTCATCGAGTCTCTCAGACCGCAGAT 1080  
Db  
1134 GCCCTGATTTATCCAGCGAGAACTTGGCTTCTCATCGAGTCTCTCGGATACGAGAGC 1193  
Qy  
1081 GAGCGTGGCTGTGCGCTCTCGGCTCTCTGGGGTCTCTCGGCGAGCCCAACCCATCCAAA 1140

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Db      1194  GAGCGGGTGTCCCGTCTCCCGCGCGGAGAGGTGCGCGCGCCCAATCCCCCAGG 1253
Qy      1141  AAGCTTCCAGACCCCGGGTCTCTGGCGGACTCCGAGACAAGGCGCTGCCGGTG 1194
Db      1254  AAGCCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 1307

RESULT 11
US-10-345-680-43
; Sequence 43, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323.
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES
; FILE REFERENCE: MPI02-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64) ... (1323)
; US-10-345-680-43

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Query Match	68.2%	Score	814.4	DB	15	Length	2772
Best Local Similarity	81.5%	Prod. No.	1.5e-233	Indels	15	Gaps	2
Matches	973	Conservative	0	Mismatches	206		
QY	1	ATGGCGACGACACACTCTGGCTCTGTGTGGCACTGTGTGCTGCTTTACTTGGTATCTGGG	60				
DB	142	ATGGCGACGACACGCTCTCTGGCCCTGCTGGCGCTGTGCTTTACTTGGTGTCTGGT	201				
QY	61	GCTCTAGTGTTCAGGCTCTGGACGCGCTCACGAGCAGCAGGCTCAGAGAGAAATGGAT	120				
DB	202	GCCCTGTGTTCGGGGCCCTGGAGCAGCCACGAGCAGCAGGCCACAGGGAGCTGGGG	261				
QY	121	CATGGCCGAGACCAATTTCTCAGGGA	CAATCCCTGTGTGAGCCAGAGAGCTCGAGGAT	180			
DB	262	GAGGTCGAGAGAAATTCCTCAGGGCCCATCCGTGTGTGAGCGACCCAGAGCTGGGCCTC	321				
QY	181	TTTCATCAGACTCCTGTTTGAAGCCCTCGGAGGGGGCGCAAAACCCAGAAACCAAGCTTGGACC	240				
DB	322	CTCATCAGAGGTTGGCTGATGCCCTCGGAGGGGGTGGGACCCAGAAACCAACTCGACC	381				
QY	241	AATAGCAGCAACCACTCATCAGCTTGGACCTCGGGCAGCGCCTTCTTTTCTTCGGGGACC	300				





; PRIOR FILING DATE: 2000-01-21							
; NUMBER OF SEQ ID NOS: 63							
; SOFTWARE: PatentIn version 3.0							
; SEQ ID NO 30							
; LENGTH: 3945							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
US-10-312-312-30							
Query Match            68.0%; Score 811.4; DB 16; Length 3945;							
Best Local Similarity 81.4%; Pred. No. 1.3e-236; Indels 15; Gaps 2;							
Matches 970; Conservative							
Qy	1	ATCGGAGACCACTCCTGGCTGTGTGGCACTGCTGTCCTTTACTTGGTATCTGGG	60				
Db	1618	ATGGCAGCACACGCTCCTGGCCCTGCTGGCGCTGGTCTTGCTTACTTGGTCTGGT	1677				
Qy	61	GCTCTAGTPTTCAGGCTCTGGAGCAGCCTCAGGAGCAGCGCTCAGAAGAAATGGAT	120				
Db	1678	GCCCTGTTGTTCCGGGCCCTGGAGCAGCCCCACGACGACGAGCCCAGAGGAGCTGGG	1737				
Qy	121	CATGGCCGACACAGATTCTTAGGGACCATCCCTGTGTGAGCCAGAAGAGCCTGGAGAT	180				
Db	1738	GAGTCCGAGAGATTCTTAGGGGCCCATCCGTGTGTGAGCAGCACGAGAGCTGGGCCCTC	1797				
Qy	181	TTCATCAAGTCTCTGTTGAAGCCCTGGAGGGGGCGAACCAGAACACAGCTGGACC	240				
Db	1798	CTCATCAAGAGGTGGCTGATGCCCTGGGAGGGGTGCGGACCCAGAAACCACTCGACC	1857				
Qy	241	AATAGCAGCAACCACTCATCAGCTCTGGAACCTGGGCAGCGCCTCTTTTTCTCGGGGACC	300				
Db	1858	AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGCAGCGCCTCTTTTCTCAGGGACC	1914				
Qy	301	ATCATCACTACCAATCGGCTATGGCAATATAGTCTTACACAGATGCGGGCGTCTCTTT	360				
Db	1915	ATCATCACCAATCGGCTATGGCAATATGGCCCTCGGCACAGATGCCGGGGCCCTCTTC	1974				
Qy	361	TGTATCTCTATGCACTGTTGGGATCCCACTGTTGCGGATGCTGTCGCGGAGTCGGG	420				
Db	1975	TGCACTCTTTATGCGCTGGTGGGATTCGCTGTTTGGGATCTACTGCGAGGGTTCGGG	2034				
Qy	421	GA CCGGCTGGGCTCTCTCTGCGCGGGGCACTGGGCCACATCGAAGCAATCTTCTTGAAG	480				
Db	2035	GACCGGCTGGGCTCTCTCTGCGGCATGGGATCGGTCACATTAAGAGCAATCTTCTTGAAG	2094				
Qy	481	TGGCATGTGCCACCGGGGCTCGTCAGAAAGTCTGTCCGCACTGCTTCTCTGTGATCGGC	540				
Db	2095	TGGCATGTGCCACCGGAGCTAAGAGTGTGTGCGCGATGCTTTTCTGTGATCGGC	2154				
Qy	541	TGCTCTCTTTTGTTCCTCACTCTCTACCTTGTGTCTCTACATGGAGAGCTCGAGCAAG	600				
Db	2155	TGCTCTCTTTTGTTCCTCACGCCCACTGTTGTGTCTGTATATGGAGAGCTCGAGCAAG	2214				
Qy	601	TTAGAGCCCATCTATTTTTATATAGTGACTCTCAACCACTGTAGGCTTTGGCGAATTATGA	660				
Db	2215	CTGGAGGCCCATCTATTTTGTCTATGTAGCGCTTACCAACCGTGGGCTTTGGCGACTATGT	2274				
Qy	661	CCGGCGATGGCAACCGGGAGAACTCTCCAGCTTACAGCGGTGTGTGTTCTTGATC	720				
Db	2275	GCCGGCGCGAACCCAGGCAGGACTCCCCGGCCTATACGCCCTGTGTGTGTTCTTGATC	2334				
Qy	721	TTGTTTGGCCTAGCCTACTTTCGCTCAGTGTCTCAACCACTCGGCAACTGGTTGCGAGCA	780				
Db	2335	CTGCTCGGCTTGCTTACTTTCGCTCAGTGTCTCAACCACTCGGCAACTGGCTCGAGTA	2394				
Qy	781	GTCTCCCGCGAACTCGGCGAGAGATGGGTGGCTTAACGGCAACAGGCTGTAGCTGGACC	840				
Db	2395	GTGTCCCGCGCACTCGGCGAGAGATGGGCGGCTTACGGCTCAGGCTGCCAGCTGACT	2454				
Qy	841	GGCACAGTGCACGGGAGTGACCCAGCGAACTGGGCCAGCGGCCCGCCCGCCAGAGAG	900				
Db	2455	GGCACAGTGCACGGCGGTGACCCAGCGAGCCGGGCCCGCCCGCCCGCGAGAGAG	2514				

601    TTAGAAGCCATCTACTTTGTTATAGTGACTCTACCACTGTAGGCTTTGGCGATTATGTA    660  
Db    2215    CTGGAGGCCATCTACTTTGTTATAGTGAAGCTTACCACTGGGGCTTTGGCGATTATGTG    2274  
QY    661    CCGCGGATGGACCGGCGAGAACTCTCCAGCTTACAGCCGCTGGTGTGGTCTCGATC    720  
Db    2275    GCCGGCGGACCCAGGAGACTCCCGGCTTATCAGCCGCTGGTGTGGTCTCGATC    2334  
QY    721    TTGTTGGCTAGCCATCTTGGCTCAGTGTCTCACCACATCGGCACATGGTTCGGAGCA    780  
Db    2335    CTGCTGGCTGGCTTACTTTCGCTCAGTGTCTCACCACATCGGGAATGCTTCGAGTA    2394  
QY    781    GTGTCGCGCGAACTCGGCGAGAGATGGTGGCTTAAGCGCACAGGCTGTAGCTGGACC    840  
Db    2395    GTGTCCCGCGCACTCGGCGAGAGATGGCGGCTTACGGCTCAGGCTGCCAGCTGGACT    2454  
QY    841    GGCACAGTGCACGCGGAGTGAACCGAGCGAACTGGGGCCAGCGCCCGCCCGCAGAGAG    900  
Db    2455    GGCACAGTGCACGCGGCGTGAACCGAGCGGCGCGCCCGCCCGCCCGCAGAGAG    2514  
QY    901    GAGCAACCACTCTCGCCCTCTCTTTGCGCGCACGCGCTGTGTTGTTGAGCCAGCCGCGC    960  
Db    2515    GAGCAGCACTGC-----TGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC    2562  
QY    961    AGGCCCGGCTCCCTGCACCCGAGAGAGGTTGAGACTCCGTCGCGCCGCCACGSCCTCA    1020  
Db    2563    AGGCCCGGATCCCTCTTCGCCCCCGAGAGGCTCAGCGCCCTTCCCGCCCGCAGCCTCG    2622  
QY    1021    GCTCTGGATTACCCCACTGAGTAATCTGGCTTCATCGACGAGTCTCTCAGACACGAGAT    1080  
Db    2623    GCCCTGGATTATCCAGCGAGAACTTGGCTTCATCGACGAGTCTCTCGGATACGAGAGC    2682  
QY    1081    GAGCGTGGCTGTGCTCCCTGCTCGGGCTCTCGGGGTCTCGCGGCGCGACCAACCATCCAAA    1140  
Db    2683    GAGCGCGGCTGCCGCTGCCCGCGCGCGAGAGTTCGCGCGCGCCAAATCCCCCAGG    2742  
QY    1141    AAGCTTCCAGACCCCGGGGTCTCGGCGACTCCGAGACAAAGGCGGTGCGG    1191  
Db    2743    AAGCCCGTGGCGCCCGCGCGCGCGCTCCCGAGACAAAGGCGGTGCGG    2793

RESULT 13  
US-10-312-312-30  
; Sequence 30, Application US/10312312  
; Publication No: US20040068097A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE  
; TITLE OF INVENTION: (LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 21272-015-061/HVS-37CIP  
; CURRENT APPLICATION NUMBER: US/10/312,312  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 09/729,739  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/488,725



QY 901 GAGCAACACTCTGCGCCTCTCTTTCCGGCAGCCGCTGCTGTTGTTGAGCAGCCGCGC 960  
Db |||||  
2515 GAGCAGCACTGC-----TGCCTCCACCGCCCTGCTCCAGCGCAGCCGCTGGGC 2562  
QY 961 AGGCCCGGCTCCCTGTCACCGCAGAGAGGTTGAGACTCCGTCGCCGCCACGGCCTCA 1020  
Db |||||  
2563 AGGCCCGGATCCCTTCGCCGCCCGAGAGAGCTCAGCGGCTTCCCGGCCACGGCCTCG 2622  
QY 1021 GCTCTGGATTACCCAGTGGAGAACTTGGCCCTTCATCGACAGTCTCTCAGACAGCAGAGT 1080  
Db |||||  
2623 GCCTGGATTATCCAGCAGAGAACCTGGCCCTTCATCGACAGTCTCTCGGATACGCAGAGC 2682  
QY 1081 GAGGTGGCTGTCGCCCTGCTCGGCTCTCGGGTCTCTCGGGTCCGCCGACCCCAACCCATCCAAA 1140  
Db |||||  
2683 GAGCGGGGCTGCGCGCTGCGCGCCGCGCCGAGAGGTGCGCGCCGCCCAAAATCCCGCCAGG 2742  
QY 1141 AAGCTTCCAGAGACCCCGGGGTCTGGGCGACTCCGAGACAAGCGCGCGC 1191  
Db |||||  
2743 AAGCCCGTGGCGGCCCGCGGCCCGCGGCTCCCGAGACAAAGCGGTGCGG 2793

## RESULT 14

US-09-747-835A-28  
; Sequence 28, Application US/09747835A  
; Patent No. US20020146692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE  
; FILE OF INVENTION: (Like) POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-37C1P  
; CURRENT APPLICATION NUMBER: US/09/747,835A  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 09/729,739  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 3996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (52)..(3996)  
US-09-747-835A-28

Query Match 68.0%; Score 811.4; DB 9; Length 3996;  
Best Local Similarity 81.4%; Pred. No. 1.3e-232;  
Matches 970; Conservative 0; Mismatches 206; Indels 15; Gaps 2;  
QY 1 ATGCGCAGCACCACTCTCGGCTCTGCTGGCACTGGTGTCTTACTTGGTATCTGGG 60  
Db |||||  
1669 ATGCGCAGCACCACTCTCGGCTCTGCTGGCCTCTGCTGGCTGCTTCTTACTTGGTGTCTGGT 1728  
QY 61 GCTCTAGTGTTCAGGCTCTGAGCAGCCTTCAGCAGCAGGCTCAGAGAGAAATGGAT 120  
Db |||||

Db 1729 GCCTCGTGTTCGCGGCCCTTGGAGCAGCCCCCAGCAGCAGAGGCCCCAGAGGAGCTGGGG 1788  
QY 121 CATGGCCGAGACACAGTTTCTGAGGGACCAATCCCTCTGTGTGAGCAGAGACCTCTGGAGGAT 180  
Db |||||  
1789 GAGGTCCGAGAGAAGTTCTGTAGGGCCCATCCGTGTGTGAGCAGCAGAGGAGCTGGGCTC 1848  
QY 181 TTCTATCAAGTCTCTGTGTTGAGGCCCTTGGAGGGGGGCGCAAAACCCAGAAACAGCTGGACC 240  
Db |||||  
1849 CTCTATCAAGGAGGTGCTGATGCCCTTGGAGGGGGGTGCGGACCCAGAAACCAATCTGCACC 1908  
QY 241 AATAGCAGCAACCACTCATCAGCTTGGAACTCTGGCAGCGCCTTCTTTTCTCTGGGGACC 300  
Db |||||  
1909 AGCAACAGCAGCCAC--TCAGCTGGACCTGGCAGCGCCTTCTTTTCTCAGGAGACC 1965  
QY 301 ATCATCACTACCACTCGGCTATGCAATATAGTCTTACACACAGATGCGGGCGCTCTTTT 360  
Db |||||  
1966 ATCATCACCACTCGGCTATGCAATATGCGCCCTGCGCACAGATGCGGGCGCCTCTTC 2025  
QY 361 TGTATCTTATGCACTGGTGGGGATCCCATCTGTTGGGATGCTGTGGGGGAGTGGG 420  
Db |||||  
2026 TGCATCTTTTATGCGCTGGTGGGGATTCGCTCTTTTGGGATCTTACTGGCAGGGGTGCGG 2085  
QY 421 GACCGCTGGGCTCCTCTCTGCGCCGGGCGCATCGGCACATCGAAGCAATCTTCTTGAAG 480  
Db |||||  
2086 GACCGCTGGGCTCCTCCTGCGCCCATGGCATCGGTACATGAGGCATCTTCTTGAAG 2145  
QY 481 TGGCATGTGCCACCGGGGCTGTGAGAAGTCTGTCCGCACTGCTCTTCTGTGATCGGC 540  
Db |||||  
2146 TGGCAGTGTCCACCGGAGCTAGTAAGAGTGTCTGCGCGATGCTTTTCTGCTGATCGGC 2205  
QY 541 TGCCTGCTTTTGTCTCTACTCTGCTGCTGCTTCTTCTACATGAGAGCTGAGCAAG 600  
Db |||||  
2206 TGCCTGCTCTTGTCTCTCAGCCACGCTTCTGCTATATGAGGAGCTGAGCAAG 2265  
QY 601 TTAGAAGCCATCTACTTTGTTAGTAGCTCTCACCACTGATGCTTTTGGCGATTATGTA 660  
Db |||||  
2266 CTGAGGCCATCTACTTTGTTAGTAGCTCTCACCACTGATGCTTTTGGCGATTATG 2325  
QY 661 CCGGGGATGGCACCGGGGAGAACTCTCCAGCCTACACGCGCTGTGTGTGTTCTGATC 720  
Db |||||  
2326 GCGCGCGGAGCCCGCAGGAGGACTCCCGGCTATCAGCGCTGTGTGTGTTCTGATC 2385  
QY 721 TTGTTTGGCTTAGCTTACTTTCGCTCAGTGTCTACACCATCGGCAACTGTTTGGAGCA 780  
Db |||||  
2386 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTACCACTATCGGAACTGGCTGCGAGTA 2445  
QY 781 GTGTCGCGCGGAACTCGGCAGAGATGGGTGGCTTAACGSCACAGGCTGTAGTGGACC 840  
Db |||||  
2446 GTGTCCCGCGCACTCGGGCAGAGATGGGCGGCTCAGGCTCAGGCTGCGAGTGA 2505  
QY 841 GGCACAGTGAACGCGAGTGAACCCAGCGAACTGGGCGCCAGCAGCCCGCGCCAGAGAG 900  
Db |||||  
2506 GGCACAGTGAACGCGCGGTGACCCAGCAGCGCGGCGCGCGCGCGCGCGCGCGAGAG 2565  
QY 901 GAGCAACCACTCTGCGCTCTCTTTTGGCGGCAACCGCTGCTGTTGTTGAGCCAGCGCGC 960  
Db |||||  
2566 GAGCAGCCACTGC-----TGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 2613  
QY 961 AGGCCCGGCTCCCTCTCACCGCAGAGAGTTGAGACTCCGTCGCCCGCCAGCGGCTCA 1020  
Db |||||  
2614 AGGCCCGGATCCCTCTTTCGCCCGCCGAGAGAGCTCAGCGGCTTCCCGCCAGCGGCTCG 2673  
QY 1021 GCTCTGGATTTACCCAGTGAAGATCTGGCCTTCATCGACAGTCTCTCAGACAGCGAGT 1080  
Db |||||  
2674 GCGCTGATTTATCCAGCGAGAACCTGGCCTTTCATCGAGAGTCTCTCGGATACGCAGAGC 2733  
QY 1081 GAGGTGGTGTGCTGCTGCTGCTGGGCTCTCTGGGGTCTCGCGCGAGCCCAACCCATCCAAA 1140  
Db |||||  
2734 GAGCGGGGTGCGCGCTGCGCGCGCGCAGAGAGTGGCGCGCGCCCAATTCGCCCGAG 2793  
QY 1141 AAGCTTCCAGACCCCGGGGTCTGGGCGACTCCGAGACAAGCGCGCTGGCG 1191  
Db |||||  
2794 AAGCCGTGCGGCGCGCGCGCGCTCCCGAGACAAAGCGGTGCGG 2844



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1194	100.0	1197	9	AY405806	Mus muscu
	2	814.4	68.2	9	AY405804	Homo sapi
	3	540	45.2	581	6	CB606856
C 4	529.6	44.4	590	2	BE981482	UI-M-CG0p
	5	517	43.3	593	2	BE981393
C 5	484.4	40.6	1560	3	CB603880	full-length
	7	420.2	35.2	469	2	BF565047
8	419.4	35.1	1405	3	BC067791	Homo sapi
	9	405.4	34.0	736	5	BA451513
10	379.2	31.8	570	2	BB569111	BB569111
	11	374.0	31.4	891	1	AK537214
C 12	340.8	28.5	822	7	CK653558	AGENCOURT
	13	318.8	26.7	922	4	BI758226
14	297.4	24.9	553	5	BM942654	UI-M-CG0p
	15	284.8	23.9	498	5	BY248534
C 16	284.4	23.8	627	7	COJ39400	UI-M-BHO-
	17	279.2	23.4	667	5	BU759620
18	259.4	21.7	613	9	AY405805	Pan trogl
	19	259.4	21.7	1745	3	AK036066
20	259.4	21.7	2534	3	AK082153	Mus muscu
	21	257.2	21.5	406	6	CB808226
22	254.8	21.3	2628	3	AK031904	Mus muscu
	23	241.4	20.2	448	5	BY252956
24	229.2	19.2	1113	9	AY418067	AY418067



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Db 298 ATCATCACACCATCGGCTATGGCAATGTGGCCCTCGGCACAGATGCCGGGCGCCTCTTC 357
Qy 361 TGTATCTTCTATGACACTGTGGGATCCCACTGTTCCGGATGCTGTGGCGGAGTCGGG 420
Db 358 TGCATCTTTTATGCGCTGTGGGATTCGCTGTTGGGATCCTACTTGGCAGGGTCGGG 417
Qy 421 GACGGCTGGGCTCTCTGTGGCGGGGATCGGCACATCAAGCAATCTTCTTGAAG 480
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Qy 481 TGCATGTGTGCACCGGGCTGTGGAGAGTCTGTCCGCACTGTCTTCTGTGATCGGC 540
Db 478 TGCACGTGTGCACCGGAGCTAGTAAGAGCTGTGTGGGATGCTTCTGTGATCGGC 537
Qy 541 TGCCTGTCTTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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Qy 601 TTAGAAGCCATCTACTTGTATAGTACTCTCACTCTCACTCTCACTCTCTCTCTCTCT 660
Db 598 CTGGAGGCCATCTACTTGTATAGTACTCTCACTCTCACTCTCACTCTCTCTCTCTCT 657
Qy 661 CCGGGGATGGCAGCGGCGAGACTCTCCAGCCTACAGCGCTGTGTGTGTGTGTGTGTGT 720
Db 658 GCGGGGCGGACCCAGCGAGACTCTCCGCGCTATCAGCGCTGTGTGTGTGTGTGTGTGT 717
Qy 721 TTGTTTGGCTAGCTACTTCTGCTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAG 780
Db 718 CTGCTCGGCTGTGCTTACTTGTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAG 777
Qy 781 GTGTCCGCGGAACTCTGGGAGAGATGGTGGCTTAACGGCAAGGCTGTAGTCTGAC 840
Db 778 GTGTCCGCGGAACTCTGGGAGAGATGGGCGGCTCAGCGCTCAGGCTCAGGCTCAGGCT 837
Qy 841 GGCACAGTGCACGGGAGTGACCCAGCAACTGGGCGGAGCGCGCGCGCGCGCGCGCGCG 900
Db 838 GGCACAGTGCACGGGAGTGACCCAGCAAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 897
Qy 901 GAGCAACCACTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 898 GAGCAGCCACTGC-----TGCTCCACCGCGCTCTCAGCGGAGCGCGCTGGGC 945
Qy 961 AGCCCGGCTCTCTCTGACCCGAGAGAGTTGAGACTCGTCTCGCGCGCGCGCGCGCGCTCA 1020
Db 946 AGCCCGGCTCTCTCTGCGCGCGCGAGAGGCTCAGCGCTTCTCTCGCGCGCGCGCGCTCG 1005
Qy 1021 GCTCTGATTTACCCAGTGAATCTGGCTTCTCAGAGGCTCTCAGAGGCTCTCAGAGGAGT 1080
Db 1006 GCGCTGATTTATCCAGAGAGAACCTGGGCTTCTCAGAGGCTCTCAGAGGAGTCTCGAGAGC 1065
Qy 1081 GAGCGTGGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
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Qy 1141 AAGCTTTCAGACCCCGGGTCTCTGGGCGACTCTCGAGACAAAGCGCGTGGCGGTG 1194
Db 1126 AAGCCGCTGGGCGCGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1179

RESULT 3
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LOCUS AMGNNUC.NRHY4-00145-C1-A W Rat hypothalamus (10464) Rattus
DEFINITION norvegicus cDNA clone nrhy4-00145-cl 5', mRNA sequence.
ACCESSION CB606856
VERSION CB606856.1 GI:29546469
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
KEYWORDS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 581)
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

Amgen EST Program.  
Amgen Rat EST Program  
Unpublished (2003)  
Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00145 row: c column: 1.

FEATURES  
source

1..581  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone\_lib="nrhy4-00145-cl"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat hypothalamus adult female Wistar rat avg. Insert size 2.3 kb fraction 6 and 7"

ORIGIN

Query Match 45.2%; Score 540; DB 6; Length 581;  
Best Local Similarity 95.7%; Pred. No. 4.1e-129;  
Matches 555; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 243 TAGCAGCAACCACTCATCAGCTTGGAACTGGGAGCGGCTCTCTTTCTCGGGGACCAT 302
Db 62 TAGCAGCAACCACTCATCAGCTTGGAACTGGGAGCGGCTCTCTTTCTCGGGGACCAT 121
Qy 303 CATCACTACCATCGGCTATGGCAATATAGTCTTACACAGATGCCGGGCGTCTCTTTTG 362
Db 122 CATCACTACCATCGGCTATGGCAATATAGTCTTACACAGATGCCGGGCGTCTCTTTTG 181
Qy 363 TATCTTTATGACATGCTGGGATGCCACTGTTCGGGATGCTGCTCGGGAGTCGGGGA 422
Db 182 TATCTTTATGACATGCTGGGATGCCACTGTTCGGGATGCTGCTGGGAGTCGGGGA 241
Qy 423 CCGGCTGGGCTCTCTCTCGCGGGGCAATCGGCACATCGAAGCAATCTTCTTGAAGTG 482
Db 242 CCGGCTGGGCTCTCTCTCGCGGGGCAATCGGTCACATCGAAGCAATCTTCTTGAAGTG 301
Qy 483 GCATGTGCCACCGGGGCTGGTGAAGTCTGTCCGAGTCTCTTCTCTGTCATCGGCTG 542
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Qy 543 CTGCTCTTTGTCTCCTCCTACCTTCTGTTCTCTACATGAGAGCTGGAGCAAGTT 602
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Qy 603 AGAGCCATCTACTTGTATAGTACTCTCACCCTGAGGCTTGGCGATTATGTACC 662
Db 422 GGAAGCCATCTACTTGTATAGTACTCTCACCCTGAGGCTTGGCGATTATGTACC 481
Qy 663 CGGCGATGCAACCGGGGCAAACTCTCCAGCTTACAGCGGCTGGTGTGGTCTGTGATCTT 722
Db 482 AGGCGATGCAACCGGGGCAAACTCTCCAGCTTACAGCGGCTGGTGTGGTCTGTGATCTT 541
Qy 723 GTTGGCTTAGGCTACTTCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCT 762
Db 542 GTTGGCTTAGGCTACTTCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCT 581
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RESULT 4  
BE981482/c  
LOCUS

DEFINITION UI-M-CGop-bdc-f-10-0-UI-s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone  
ACCESSION BE981482  
VERSION BE981482.1 GI:10650633  
KEYWORDS EST.

[illegible]

FEATURES	source
Location/Qualifiers	
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/strain="C57BL/6J"	
/db_xref="taxon:10090"	
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/lab_host="DH10B (Life Technologies)"	
/clone_lib="NIH BMAP Ret4 S2"	
/note="Vector: pV7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at <a href="http://brainest.eng.utoro.edu">brainest.eng.utoro.edu</a> . The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine	

ORIGIN	TAG_SEQ=None found"	division of Invitrogen.	FEATURES	source
Query Match	43.3%; Score 517; DB 2; Length 593;	Location/Qualifiers		
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		/db_xref="taxon:9606"		
		/clone="CS0DF019YL24"		
		/tissue_type="Fetal brain"		
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ORIGIN				
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Db	554 ATGGCGAGCACCACATCTCTGGCTCTGCTGGCACTGGTGTCTTACCTTGGTATCTGGG 495	595 CCATCCCGCAGAGTGGCAGCTGCCACCGGAGCTAGTAGAGTGTCTGGCGCATGCTTT 654		
Qy	61 GCTCTAGTGTCCAGGCTCTGGAGCAGCTTCCAGCAGCAGCTCAGAGAAATGGAT 120	527 TCCTGTGATCGGCTGCTCTTGTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 586		
Db	494 GCTCTAGTGTTCAGGCTCTGGAGCAGCTTCCAGCAGCAGCTCAGAGAGAGTGGAT 435	655 TCCTGTGATCGGCTGCTCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 714		
Qy	121 CATGGCGCAGACCACTTCTTGAGGAGCATTCCCTGTGTGAGCAGAGAGCTCTGGAGGAT 180	587 AGAGCTGGAGCAGTGTAGAGCCATCTACTTGTGTATAGTACTCTCACCACCTGAGGCT 646		
Db	434 CATGGCGCAGACCACTTCTTGAGGAGCATTCCCTGTGTGAGCAGAGAGCTCTGGAGGAT 375	715 AGAGCTGGAGCAGTGTAGAGCCATCTACTTGTGTATAGTACTCTCACCACCTGAGGCT 774		
Qy	181 TTCAATCAAGCTCTCTGGTTGAAGCCCTGGGAGGGGGCGCAAAACCCAGAAACACAGCTGAC 240	647 TTGGCCATTATGTACCCCGCATGGCAGCGGCGAGAACTCTCCAGGCTTACAGCCGCTGG 706		
Db	374 TTCAATCAAGCTCTCTGGTTGAAGCCCTGGGAGGGGGCGCAAAACCCAGAAACACAGCTGAC 315	775 TTGGCCATTATGTACCCCGCATGGCAGCGGCGAGAACTCTCCAGGCTTACAGCCGCTGG 834		
Qy	241 AATAGCAGCAACCACTCATCAGCTTGGAACTGGAGCGGCGCTTCTTTTCTCGGGGACC 300	707 TGTGTTCTTGGATCTTGTGTGGCTAGCTTACTTCTGCTCTAGTGTCTCACCACCATGGCA 766		
Db	314 AATAGCAGCAACCACTCATCAGCTTGGAACTGGAGCGGCGCTTCTTTTCTCGGGGACC 255	835 TGTGTTCTTGGATCTTGTGTGGCTAGCTTACTTCTGCTCTAGTGTCTCACCACCATGGCA 894		
Qy	301 ATCATCACTACCTATGCTATGCAATATAGTCTTACACACAGATGCCGGGCGCTCTCTTT 360	767 ACTGTTGGAGCAGTGTCCCGCACTCGGGCAGAGATGGGTGGCTTAAACGGCAGG 826		
Db	254 ATCATCACTACCTATGCTATGCAATATAGTCTTACACACAGATGCCGGGCGCTCTCTTT 195	895 ACTGTTGGAGCAGTGTCCCGCACTCGGGCAGAGATGGGTGGCTTAAACGGCAGG 954		
Qy	361 TGTATCTTCTATGCTATGCTGGGATCCCACTGTTGGGATGCTGTGGCGGAGTCGGG 420	827 CTGCTAGCTGGACCGGCGCAGACAGTGCAGCGAGTGCACCCAGCGAACTGGGCGCAGCGGCC 886		
Db	194 TGTATCTTCTATGCTATGCTGGGATCCCACTGTTGGGATGCTGTGGCGGAGTCGGG 135	955 CTGCTAGCTGGACCGGCGCAGACAGTGCAGCGAGTGCACCCAGCGAACTGGGCGCAGCGGCC 1014		
Qy	421 GACGGCTGGGCTCTCTCTGCGCGGGGATGGAGAGTCTGT-CGCGAGTGTCTTTC 528	887 CGCGCGCAGAGAGAGCAACCACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 946		
Db	134 GACGGCTGGGCTCTCTCTGCGCGGGGATGGAGAGTCTGT-CGCGAGTGTCTTTC 75	1015 CGCGCGCAGAGAGAGCAACCACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1062		
Qy	481 TGGCATGTGTCACCGGGGCTGGTGAAGTCTGT-CGCGAGTGTCTTTC 26	947 TTGAGCAGCGCGCAGCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1006		
RESULT 6				
CR603880				
LOCUS	1560 bp mRNA linear HTC 21-JUL-2004			
DEFINITION	full-length cDNA clone CS0DF019YL24 of Fetal brain of Homo sapiens (human).			
ACCESSION	CR603880			
VERSION	CR603880.1 GI:50484687			
KEYWORDS	HTC; CNSLT cDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Redwood City, CA 94063			
REFERENCE	2 (bases 1 to 1560)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)			
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a			

RESULT 7

BF565047

LOCUS

DEFINITION

BF565047 469 bp mRNA linear EST 12-DEC-2000  
UI-R-B01-ajm-g-02-0-UI.r1 UI-R-B01 Rattus norvegicus cDNA clone  
UI-R-B01-ajm-g-02-0-UI 5', mRNA sequence.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 168 Row: 0 Column: 5



This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718766  
This clone has the following problem: retained intron.

## FEATURES

source  
1. 1405  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/lab\_host="DH10B"  
/note="vector: pBluescript"

## ORIGIN

Query Match 35.1%; Score 419.4; DB 3; Length 1405;  
Best Local Similarity 69.6%; Pred. No. 1.1e-97;  
Matches 697; Conservative 0; Mismatches 141; Indels 163; Gaps 3;

QY 194 TGGTTGAAGCCCTGGGAGGGGGCGCAAAACCCAGAAACCACTGGACCAATAGCAGCAACC 253  
DB 247 TGGCTGATGCCCTGGGAGGGGGTGGGACCCAGAAACCACTGGACCAACAGCAGGCC 306  
QY 254 ACTCATCAGCTTGAACCTGGGAGCGCTTCTTTTCTCGGGACCATCATCACTACCA 313  
DB 307 AC---TCAGCCTGGGACCTGGGAGCGCCCTCTTTTCTCAGGAGCAATCATCACCACCA 363  
QY 314 TCGGCTATGGCAATATAGTCTTACACAGATGCGGGCGCTCTTTTGTATCTTCTATG 373  
DB 364 TCGGCTATGGCAATATGCGCTTGGGACAGATGCGGGCGCTCTTCTGCACTTTTATG 423  
QY 374 CACTGTGGGATCCCACTGTTCCGGATGCTGTGGCGGAGTCGGGACCGCTGGGCT 433  
DB 424 CGCTGTGGGATTCGCTGTTTGGGATCTTACTGTGGGAGTGGGACCGCTGGGCT 483  
QY 434 CTTCTGTGGCGGGGACCTGGGACCATCAAGCAATCTTCTGAAGTGCATGTGCCAC 493  
DB 484 CTTCTGTGGCGGACCTGGGACCATCAAGCAATCTTCTT-----526  
QY 494 CGGGGCTGGTGAAGAGTCTGCGCAGTGTCTTCTGCTGATCGGCTGCTGCTCTTTG 553  
DB 527 -----526  
QY 554 TCCTCACTCTACTCTTGTGTTTCTCTACATGGAGAGCTGGAGCAAGTTAGAGCCATCT 613  
DB 527 -----526  
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DB 527 -----GTGACGCTTACCACCGTGGGCTTTGGCGACTATGTGGCGGCGGAGCC 575  
QY 674 CCGGGCAGAACTCTCCAGCCTACAGCGCTGTGTGTGTTCTCGATCTTGTGCTGTAG 733  
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QY 734 CTTACTTGGCTCAGTGTCTCACCACCATCGGCAACTGGTTGCGAGAGTGTCCCGCGAA 793  
DB 636 CTTACTTGGCTCAGTGTCTCACCACCATCGGCAACTGGCTGCGAGTAGTGTCCCGCGCA 695  
QY 794 CTGGGAGAGATGGTGGCTTAACGGCAGCAGCTGTAGCTGGACCGGACAGTGCACAG 853  
DB 696 CTGGGAGAGATGGGCGGCTTACCGCTCAGGCTGCTGCTGAGTGGCAGAGTGCACAG 755  
QY 854 CGGAGTGCACCGCAACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 913  
DB 756 CGGCGTGCACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 815  
QY 914 TGCCCTCTCTTTTCCGCGCACCGCTCTGTGTGTGAGCCAGCGGCGGCGGCGGCTCCC 973  
DB 816 -----TGCCCTCCACCGCTCTGTGTGTGAGCCAGCGGCTGGGCGGCGGCGGCGG 863  
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DB 864 CTTTGGCCCCCGAGAGAGGCTCAGCCGCTTCCCGCGGCGGCTCGGCCCTGGATTATC 923  
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DB 924 CCAGCGAGAACTTGGCTTTCATCGACGAGTCTCTCGATAGCAGAGCGAGCGGCTGCC 983  
QY 1094 CCTGTGCTGGGCTCTCTGGGGTTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1153  
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QY 1154 CCGCGGCGCTCTGGGCGGACTCCGAGACAGCGCGTGCCTGGT 1194  
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## RESULT 9

BX451513

## LOCUS

736 bp mRNA linear EST 06-MAY-2004  
BX451513 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CSODF019YL24 5-PRIME, mRNA sequence.

## ACCESSION

BX451513

## VERSION

BX451513.2

## KEYWORDS

GI:47063398

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polaves, D.

## TITLE

Full-length cDNA libraries and normalization

## JOURNAL

Unpublished (2001)

## COMMENT

On May 22, 2003 this sequence version replaced gi:31026267.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 6303.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?e=CS0BAF015ZF10\_AF01423\_l&amp;c=6303.f

## FEATURES

source

Location/Qualifiers

1. 736

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODF019YL24"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

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/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

## ORIGIN

Query Match 34.0%; Score 405.4; DB 5; Length 736;  
Best Local Similarity 80.3%; Pred. No. 4.1e-94;  
Matches 505; Conservative 0; Mismatches 111; Indels 13; Gaps 2;

QY 566 CTTTCTGTTTCTCTACATGGAGAGCTGGAGCGAGTAGAGCCATCTACTTTTATAG 625

DB 7 CGTTCTGTTTCTCT-TATGGAGAGCTGGAGCAAGCTGGAGGCCATCTACTTTTGTATAG 65

QY 626 TGACTCTCACCAGTGTAGGCTTTGGCGATTATGTACCCGCGATGGACCGGCGAGAACT 685

DB 66 TGACGCTTACCACCTGGGCTTTGGCGACTATGTGTGCGCGGCGGACCCAGGAGACT 125

[illegible]

RESULT 10

BB569111 linear EST 26-OCT-2001

BB569111 570 bp mRNA

LOCUS

BB569111 RIKEN full-length enriched, 17 days embryo head Mus

DEFINITION

musculus cDNA clone 3322402C04 5', mRNA sequence.

ACCESSION

BB569111

VERSION

BB569111.2 GI:16449181

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 570)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

AUTHORS

Unpublished (2001)

TITLE

On Nov 29, 2001 this sequence version replaced gi:11460019.

JOURNAL

Contact: Yoshihide Hayashizaki

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Sueniro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome.res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Suganara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res* 10 (10): 1617-1630 (2000)

wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES	Location/Qualifiers
source	1..570 organism="Mus musculus" mol_type="mRNA" strain="C57BL/6J" db_xref="taxon:10090" clone="3322402C04" sex="mixed" tissue.type="head" dev_stage="17 days embryo" lab_host="rHLI08" clone_lib="RIKEN full-length enriched, 17 days embryo head"
ORIGIN	/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGATCTCGAGTAAATAATTATCCGCCCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAAGATCTCGAGTAAATAATTATCCGCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
Query Match	31.8%; Score 379.2; DB 2; Length 570;
Best Local Similarity Matches 384; Conservative	98.0%; Pred. No. 2.5e-87; Indels 0; Gaps 0;
QY	803 AGATGGGTGCCTAAACGCGACAGCGTGCTAGCTGGACCGGACACAGTCAGCACAGCGCGAGTGA 862
Db	123 AGATGGGTGCCTAAACGCGACAGCGTGCTAGCTGGACCGGACACAGTCAGCACAGCGCGAGTGA 182
QY	863 CCCAGCGAACTGGGCCAGCGCCCGCCGCGCAGAGAAGGACCACTCTCTCCCTCCT 922
Db	183 CCCAGCGAACTGGGCCAGCGCCCGCCGCGCAGAGAAGGACCACTCTCTCCCTCCT 242
QY	923 CTTTTCGCGGACACCGCTGCTGTGTTTCAGCGACGCGCGACGCCGGTCCCTCTGCACCCG 982
Db	243 CTTTTCGCGGACACCGCTGCTGTGTTTCAGCGACGCGCGACGCCGGTCCCTCTGCACCCG 302
QY	983 CAGAGAAGTTTGAGACTCCGTCCTCCCGCCACAGCGCTCAGCTCTGGATTATCCCAAGTCAGA 1042



/issue type="testis, pooled"  
 /lab host="NIH MGC 237"  
 /note="Organ: testis; Vector: pExpress-1; Site 1: EcorV;  
 Site 2: NotI; RNA obtained from testis tissue of 8 wk old  
 animal. Tissues were snap-frozen and kept at -80C before  
 RNA extraction and purification (Tri-reagent method). cDNA  
 was primed using oligo-dT primer:  
 5'-pGACTAGTCTGATCGGAGCGGCCCT(7)25-3' and cloned into  
 the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb  
 resulted in an average insert size of 2.4 kb. This primary  
 library is not normalized (normalized primary library is  
 NIH MGC 238) and was constructed by Express Genomics  
 (Frederick, MD)"

ORIGIN

Query Match 28.5%; Score 340.8; DB 7; Length 822;  
 Best Local Similarity 93.6%; Pred. No. 2.6e-77;  
 Matches 367; Conservative 0; Mismatches 22; Indels 3; Gaps 1;

803 AGATGGTGGCTTAACGGCAAGCTGTCTAGCTGGACCGGCAAGTGCAGCGCGAGTGA 862  
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 863 CCCAGCAACTGGGCCCGCCGCGCCGCGCCGAGAGGAGCAACCACTCTCCCTCT 922  
 201 CCCAGCAACTGGGCCCGCCGCGCCGCGCCGAGAGGAGCAACCACTCTCCCTCT 260  
 923 CTTTGGCGGCAACCGCTGTCTGTGTGAGCGAGCGCGCCGCTCCCTGCAACCG 982  
 261 CTTTGGCGGCAACCGCTGTCTGTGTGAGCGAGCGCGCCGCTCCCTGCAACCG 320  
 983 CAGAGAGGTTGAGCTCTCGTCCCGCGCCGCGCTCAGCTCTGATACCCAGTGA 1042  
 321 CAGAGAGGTTGAGCTCTCGTCCCGCGCCGCGCTCAGCTCTGATACCCAGTGA 377  
 1043 ATCTGGCTTCTATCGACGAGTCTCAGACGCGAGAGTGGCTGTGCTCGCTC 1102  
 378 ATCTGGCTTCTATCGACGAGTCTCAGACGCGAGAGTGGCTGTGCTCGCTC 437  
 1103 GGGCTCTCTCGGGGTGCGCCGCGCCGCGCCGAGTCCAGAGCTTCCAGAGCGGGGTC 1162  
 438 GTGCGCTCTCGGGGTGCGCCGCGCCGCGCCGAGTCCAGAGCTTCCAGAGCGGGGTC 497  
 1163 CTGGCGGAGTCCGAGCAAGCGCGTGGCGGTG 1194  
 498 CTGGCGGAGTCCGAGCAAGCGCGTGGCGGTG 529

RESULT 13  
 BI758226 922 bp mRNA linear EST 25-SEP-2001  
 LOCUS 603029871F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5200313 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI758226  
 VERSION BI758226.1 GI:15749804  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 922)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: L1AM1501 row: m column: 18  
 High quality sequence stop: 785.  
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 source 1..922  
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 /clone lib="NIH\_MGC\_114"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: EcorV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (EcorV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 019. Note:  
 this is a NIH\_MGC Library."

ORIGIN

Query Match 26.7%; Score 318.8; DB 4; Length 922;  
 Best Local Similarity 82.0%; Pred. No. 1.4e-71;  
 Matches 392; Conservative 0; Mismatches 82; Indels 4; Gaps 2;

1 ATGCGCAGCACAC-ATCTCTGGCTCTGCTGGCACTGGTCTGCTTACTTGGTATCTGG 59  
 134 ATGCGCAGCACACATGCTCTCTGGCCCTGCTGGCTCTTGTCTTACTTGGTCTGG 193  
 60 GGCTCTAGTGTTCAGGCTCTGGAGCGCTCAGCAGCAGCAGCTCAGAGAAATGGA 119  
 194 TGCCCTGTGTTCGGGCGCTGGAGCAGCCCAAGCAGCAGCAGCAGGAGGAGCTGGG 253  
 120 TCATCGCGCAGACCACTTCTGAGGAGCCATCCCTGTGTGAGCCAGAGAGCTTGAGGA 179  
 254 GGAGGTCCGAGAGAGTTCCTGAGGCGCCATCCGTGTGTGAGCGACCAAGAGCTGGGCT 313  
 180 TTTCTATCAAGCTCTGTTGAAGCCCTGGAGGGGCGCAACCCAGAGAAACAGCTGGAC 239  
 314 CCTCATCAAGAGGTTGGCTGATGCTGCGGAGGGGGTGGACCCAGAGAAACCACTGCAC 373  
 240 CAATAGCAACCACTCATCATGTTGGAACCTGGGAGCGCTTCTTTTCTCGGGGAC 299  
 374 CAGCAACAGCGCAC---TCAGCTGGACCTGGGAGCGCTTCTTTTCTCAGGGAC 430  
 300 CATCATCACTACATCGGCTATGGCAATATAGTCTTACACAGATGCGGCGCTCTTT 359  
 431 CATCATCACTACATCGGCTATGGCAATATGGCCCTGGGCAAGATGCGGCGCTCTTT 490  
 360 TTGTATCTTATGCACTGTGGGATCCACTGTTTGGGATGCTGTGGCGGAGTCTGG 419  
 491 CTGCATCTTTTATGCGCTGTGGGATTCGCTGTTTGGATCTTACTTGGCAGGGGTGG 550  
 420 GGACCGGCTGGGCTCTCTCTGCGCGGGGATTCGCGCCATCGAGAGCAATCTTTT 477  
 551 GGACCGGCTGGGCTCTCTCTGCGCGCATCGGCTCAGATTGAAGCCATCTTTCTT 608

RESULT 14  
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 LOCUS BM942654  
 DEFINITION UI-M-CGOp-bdb-f-11-0-UI.r1 NIH BMAP Ret4\_S2 Mus musculus cDNA clone  
 UI-M-CGOp-bdb-f-11-0-UI 5', mRNA sequence.  
 ACCESSION BM942654  
 VERSION BM942654.1 GI:19402517  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 553)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.

**TITLE** Normalization and subtraction: two approaches to facilitate gene discovery

**JOURNAL** Genome Res. 6 (9), 791-806 (1996)

**MEDLINE** 97044477

**PUBMED** 889548

**COMMENT** Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov  
Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of Medicine  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 REVERSE.

**FEATURES**

source

1. 553  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/clone\_lib="NH BMAP Ret4 S2"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NH BMAP Ret4 S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine"

**ORIGIN**

Query Match 24.9%; Score 297.4; DB 5; Length 553;  
Best Local Similarity 96.5%; Pred. No. 4.4e-66;  
Matches 304; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 239 ATGCGCAGCACCACCTCTGGCTGCTGGCACTGGTGTCTTACTTGGTATCTGGG 298  
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QY 61 GCTCTAGTGTTCAGGCTCTGGAGCGCCTCAGCAGCAGCGCTCAGAGAAATGGAT 120  
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Db 299 GCTCTAGTGTTCAGGCTCTGGAGCGCCTCAGCAGCAGCATGCTCAGATAAATGGAT 358  
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QY 121 CATGGCGGAGCAGCAGTCTTCAGGGACCATCCTGTGTGAGCCAGAGAGCCTGGAGGAT 180  
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Db 359 CATGGTGGAACTAGTCTTCAGGGACCATCCTGTGTGAGCCAGAGAGCCTGGAGGAT 418  
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QY 181 TTCTCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGGGCCAAACCCAGAAACCTGGACC 240  
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Db 419 TTCTCAAGCTCTCTGGTTGAAGCCCTGGAGGGGGGGCCAGCCAGAACCTGGACC 478  
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QY 241 AATAGCAGCAACCACTCATCAGCTTGAACTGGAGCGAGCCCTCTTTTCTCGGGGACC 300  
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QY 301 ATCATCACTACCATC 315  
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Db 539 ATCATCACTACCATC 553  
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**RESULT 15**

BY248534  
LOCUS BY248534 RIKEN full-length enriched, visual cortex Mus musculus  
DEFINITION

**ACCESSION**  
BY248534  
**VERSION**  
BY248534.1  
**KEYWORDS**  
EST.  
**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**

**REFERENCE**  
AUTHORS

CDNA clone K230317009 5', mRNA sequence.

BY248534

GI:26430046

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 498)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Otao, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

Cariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,

Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, W.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Michela Fagioli and Takao K. Hensch (

Laboratory for Neuronal Circuit Development Brain Science Institute

RIKEN 2-1 Hirosewa,Wako-shi,Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES  
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/tissue type="visual cortex"  
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ORIGIN

Query Match 23.9%; Score 284.8; DB 5; Length 498;  
Best Local Similarity 97.6%; Pred. No. 8.2e-63;  
Matches 289; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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Qy 61 GCTCTAGTGTCCAGGCTCTGGAGCCCTCACGAGCAGCAGCTCAGAGAAATGGAT 120  
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Qy 261 GCTCTAGTGTCCAGGCTCTGGAGCCCTCACGAGCAGCAGCTCAGAGAAATGGAT 320  
Db |||||||  
Qy 121 CATGCCGAGACGAGTTTCTGAGGGACCATCCCTGTGTGAGCCAGAGAGCCTGGAGGAT 180  
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Qy 441 AATAGCAGCAACCACTCATCAGCTTGAACCTGGGAGCGCCTTTTTTTTGGG 496  
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Job time : 4243 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 20:30:41 ; Search time 5607.24 Seconds  
(without alignments)  
3356.607 Million cell updates/sec

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Perfect score: 2079  
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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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DEFINITION Sequence 1 from Patent WO9945108.  
ACCESSION AX018705  
VERSION AX018705.1 GI:10042825  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS Pink, M., Honore, E., Duprat, F., Lesage, F. and Lazdunski, M.  
TITLE Novel mechanically sensitive mammal potassium channel family  
activated by polyunsaturated fatty acids and their use particularly  
for screening medicines  
JOURNAL Patent: WO 9945108-A 1 10-SEP-1999;  
PINK MICHEL (FR); HONORE ERIC (FR); DUPRAT FABRICE (FR); LESAGE  
FLORIAN (FR); CENTRE NAT RECH SCIENT (FR); LAZDUNSKI MICHEL (FR)

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DB	404	CATGGCGGAGACCACTTCCTGGAGGACCATCCCTGTGTGAGCCAGAGAGCTTGGAGAT	463
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DB	524	AATAGCAGCAACCACTCATCAGCTTGAACCTGGCAGCGCCCTCTTTCTCGGGGACC	593
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DB	644	TGTATCTTTCATGCTGGTGGGATCCCACTGTTCGGGATGCTGTGGCGGAGTCGGG	703
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DB	824	TGCTGTCTTGTGCTCTCTCTACCTCTGCTGTCTCTACATGAGAGCTGGAGCAAG	893
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DB	884	TTAGAGCAATCTACTTTGTATAGTACTCTACCACTGTAGGCTTGGCGATTATGTA	943
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DB	944	CCGGCGATGGCACCGGGCAGAACTCTCCAGCCTTACCAGCGCTGGTGTGCTGATC	1003
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QY	301	GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly	320
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QY	341	AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer	360
DB	1304	GCTCTGGATTACCCCACTGAGAACTTGGCTCTTCATCGAGAGTCTTCAGACACGAGAT	1363
QY	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys	380
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QY	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398
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DEFINITION		Mus musculus TRAAK K+ channel subunit mRNA, complete cds.	
ACCESSION	AF056492		
VERSION	AF056492.1	GI:3329456	
KEYWORDS			
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
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AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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JOURNAL		Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M. and Lazdunski, M.	
MEDLINE		A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids	
PUBMED		EMBO J. 17 (12), 3297-3308 (1998)	
REFERENCE		98292450	
AUTHORS		6228867	
TITLE		2 (bases 1 to 1795)	
JOURNAL		Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M. and Lazdunski, M.	
Direct Submission			
Submitted (01-APR-1998)		Institut de Pharmacologie Molculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Valbonne 06560, France	
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QY	41	HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp	60
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QY	101	IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyVargLeuPhe	120
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DB	704	GACCGCTGGCTCTCTCTGCGCGGGGATCGGCCACATCGCAACATCTCTTTGAG	763
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DB	824	TGCTGTCTTGTCTCTCACTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	883
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DB	884	TTAGAAGCCATCTACTTGTGTATAGTACTCTACCACTGTAGGCTTGGCGATTATGTA	943
QY	221	ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle	240
DB	944	CCCGCGGATGGCACCGGCGAAGTCTCCAGCCTACCAAGCGCTGGTGTGGTCTCGATC	1003
QY	241	LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla	260
DB	1004	TTGTTTGGCTTACCTACTCTGCTTACGTCTACCACTACCACTCGGCACTGGTTCGAGCA	1063
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QY	281	GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys	300
DB	1124	GGCAGAGTGCACAGCGAGTGTACCCAGCGAACTGGGCGCCAGCGCCCGCCAGAGAG	1183
QY	301	GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly	320
DB	1184	GAGCAACCACTCTCTGCT	1243
QY	321	ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer	340

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QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
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QY 61 PheileLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
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DB 361 TGTATCTTCTATGCTGCTGGGATCCCACTGCTCGGGATGCTGCTGGCTGGAGTCGG 420
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 421 GACCGGCTGGGCTCTCTCTGCGCCGGGGCATCGGTACATCGAAGCAGTTTCTTGAAG 480
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DEFINITION Sequence 1 from patent US 6426197.
ACCESSION AR221261
VERSION AR221261.1 GI:23328170
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Unclassified.
TITLES 1 (bases 1 to 1182)
Duckworth, D.M. and Chapman, C.G.
POLYNUCLEOTIDES encoding a human potassium channel
JOURNAL Patent: US 6426197-A 1 30-JUL-2002;
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VERSION AX250709.1 GI:15984447  
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ORGANISM Homo sapiens  
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AUTHORS Lazdunski, M., Lesage, P. and Maingret, F.  
TITLE Novel family of mechanically sensitive human potassium channels  
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AX278168.1 GI:16605322
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Glucksmann, M.A.
AUTHORS
12303, a novel human twik molecule and uses thereof
TITLE
Patent: WO 0177329-A 3 18-OCT-2001;
JOURNAL
MILLENIUM PHARMACEUTICALS, INC. (US)
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Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
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## ORIGIN

## Alignment Scores:

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Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: Gaps: 2

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US-09-655-272-2 (1-398) x AX278166 (1-1408)

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DEFINITION cds.
ACCESSION AF248242
VERSION AF248242.1 GI:11139499
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1544)
AUTHORS Chapman,C.G., Meadows,H.J., Godden,R.J., Campbell,D.A.,
Duckworth,M., Kelsell,R.E., Murdock,P.R., Randall,A.D., Rennie,G.I.
and Gloger,I.S.
TITLE Cloning, localisation and functional expression of a novel human,
cerebellum specific, two pore domain potassium channel
JOURNAL Brain Res. Mol. Brain Res. 82 (1-2), 74-83 (2000)
MEDLINE 20499203
PUBMED 11042359
REFERENCE 2 (bases 1 to 1544)
AUTHORS Chapman,C.G. and Duckworth,M.D.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Biotechnology & Genetics, SmithKline
Beecham Pharmaceuticals, New Frontiers Science Park (North), Third
Avenue, Harlow, Essex CM19 5AW, UK
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ORIGIN

Alignment Scores:  
Pred. No.: 1.9e-66 Length: 1544  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 9 Gaps: 2

US-09-655-272-2 (1-398) x AF248242 (1-1544)

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Db	481	GAGGTCCGAGAGAGTCTCTGAGGGCCCATCCGTGTGTGAGCGACACGAGGAGCTG	540
Qy	61	PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaIleAlaIleProGluThrSerTyrThr	80
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Qy	181	CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTyrSerLys	200
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Qy	201	LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal	220
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Qy	261	ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaIleSerTyrThr	280
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Ozaita.A. and Vega-Saenz de Miera,E.			
Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human			
two-pore K+ channel gene KCN4. Chromosomal localization, tissue			
distribution and functional expression			
Brain Res. Mol. Brain Res. 102 (1-2), 18-27 (2002)			
2 (bases 1 to 1730)			
Ozaita.A. and Vega-Saenz de Miera,E.C.			
Direct Submission			
Submitted (21-APR-2000) Physiology and Neuroscience, New York			
University School of Medicine, 550 First Avenue, New York, NY			
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ORIGIN			



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ACCESSION AF247042  
VERSION AF247042.1 GI:7576934  
KEYWORDS Homo sapiens (human)  
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Gray, A.T.  
Assignment of KCNK4 encoding the human potassium channel TAAK to  
chromosome 11  
Unpublished  
2 (bases 1 to 2772)  
Gray, A.T.  
Direct Submission  
Submitted (21-MAR-2000) Anesthesia, Room S 261, UC San Francisco,  
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Pred. No.: 3 41e-66 Length: 2772  
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Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 9 Gaps: 2

US-09-655-272-2 (1-398) x AF247042 (1-2772)

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 181489)  
 Birren, B., Nusbaum, C. and Lander, E.  
 Mus musculus chromosome 19, clone RP24-493B6  
 Unpublished  
 2 (bases 1 to 181489)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,  
 Boukhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,  
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,  
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Faros, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karatas, A., Kells, C., Lakocue, K., Lamazares, R.,  
 Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,  
 MacLean, C., Macdonald, P., Major, J., McKernan, K., Meldrum, J., Meneus, L.,  
 McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,  
 Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,  
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,  
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (08-MAY-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 181489)  
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
 Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,  
 Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,  
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faros, S.,  
 Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W.,  
 Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C.,  
 Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C.,  
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
 Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,  
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
 Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
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 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
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 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (18-JUN-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 4 (bases 1 to 181489)  
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
 Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,  
 Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,  
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faros, S.,  
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 Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C.,  
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 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
 Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
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 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
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 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (26-JUL-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 5 (bases 1 to 181489)  
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
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 Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W.,  
 Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C.,  
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 Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,  
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 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
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 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,  
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (26-JUL-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

Rachupka, A., Ranasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (01-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jul 26, 2003 this sequence version replaced gi:31880200.  
 All repeats were identified using RepeatMasker:  
 Smit, A.P.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIFR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information  
 Center project name: L26033  
 Center clone name: 493\_E\_6  
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## FEATURES

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US-09-655-272-2 (1-398) x AC120557 (1-181489)

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 Db 82982 AGCAGCAACCACTCATCAGCTTGGAACTGGGCGGCGCTCTTTTCTCGGGACCATC 83041  
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83462	AGAGGGT	GAGAGATGAATTGTTAGTTACTGGCATCTCAATGGCTCTATCTCCACCC	83521	84542	TTTGTAA	GACGACGAGATCAGGAGGATTGCTGCGAGTTTAGACTTTGCTGGGTTATAGA	84601
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247	eAlaSer	ValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArgThrArgAl	267	369	laProArg	GlyArgArgProAsnProSerLysLysProSerArgProArgGlyProG	389
84182	CGCCTC	AGTGTCTACCCACCATCGGCACTGGTTGCGAGCAGTGTCCCGCCGAACTCGGGC	84241	85262	CTCCTC	GGGGTTCGCCCGCCAGCCCAACCCATCCAAAAGGCTTCCAGACCCCGGGTCTCTG	85321
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XX Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;  
PI  
XX WPI; 1999-551038/46.  
DR P-PSDB; AAY30647.  
XX  
XX New mechanically sensitive potassium channel, used to screen for specific  
PT modulators, potential therapeutic agents for heart and nervous system  
PT disorders.  
PT  
XX  
PS Claim 6; Fig 1; 40pp; French.  
XX  
XX The present sequence encodes a mechanically sensitive potassium channel  
CC protein designated TRAAK. The protein is activated by polyunsaturated  
CC fatty acids, particularly arachidonic acid, and by riluzole. The protein  
CC is used to screen for specific modulators which are useful for treating  
CC or preventing diseases of the heart and nervous systems in humans and  
CC animals, e.g. epilepsy, cardiovascular disease (arrhythmia),  
CC neurodegeneration (particularly where associated with ischemia or  
CC anoxia), abnormalities of hormone secretion and muscular disease. The  
CC protein itself may be used to treat these diseases. Antibodies specific  
CC for the protein are used to detect it in tissues, also as therapeutic  
CC inhibitors or activators  
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Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
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US-09-655-272-2 (1-398) x AAZ10606 (1-1794)

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QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGly 180  
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DB 1184 GAGCAACCACTCTGTGCTCTTTCGCGCACCGCTGTGTGTGTGAGCCAGCCGGC 1243  
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340  
DB 1244 AGGCGCGGCTCCCTTGCCACCGCAGAGAGGTTGAGACTCCGTCCCGCCCGCCCTCA 1303  
QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
DB 1304 GCTCTGGATTACCCAGTGAGAACTCTGGCTTCATCGACGAGTCTCTCAGACCGCAGAT 1363  
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgAlaProAsnProSerLys 380  
DB 1364 GAGCGTGGGTGTGCTCTGCGGCTCTCTGGGCTCGCCCGGACCCCAACCCATCCAA 1423  
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
DB 1424 AAGCCTTCAGACCCCGGGTCTCTGGGACTCTCCGAGACMAAGCGGTGCCGTG 1477

RESULT 2  
AAA27105  
ID AAA27105 standard; cDNA; 1182 BP.  
XX  
XX AAA27105;  
AC  
XX  
XX 04-AUG-2000 (first entry)  
XX  
XX Human h-TRAAK cDNA sequence #1.  
XX  
XX Human; h-TRAAK; potassium channel polypeptide;  
XX 2P domain potassium channel; neurodegenerative disease; stroke;  
XX psychiatric disorder; neurological disorder; Gene therapy; ss.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..1182  
XX /tag= a  
XX /product= "h-TRAAK protein #1"  
XX  
XX WO200026253-A1.  
XX  
XX 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-GB003634.  
XX  
XX 03-NOV-1998; 98GB-00024048.  
XX  
XX 07-OCT-1999; 99GB-00023668.  
XX  
XX



XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Chapman CG, Duckworth DM;  
 XX WPI; 2000-365583/31.  
 DR P-PSDB; AAY94425.  
 XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of h-TRAAK  
 PT related disorders, e.g. depression and schizophrenia.  
 XX Claim 5; Page 21; 35pp; English.  
 XX Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK  
 CC polynucleotides from human tissue samples. h-TRAAK polypeptides have  
 CC homology to the 2p domain potassium channel family of polypeptides. The h  
 CC -TRAAK polypeptides and polynucleotides may be used in diagnostic assays  
 CC for conditions related to h-TRAAK imbalance and for identifying agonists  
 CC and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and  
 CC polynucleotides may also be useful for treatment and prevention (e.g. as  
 CC vaccines) of certain diseases, such as pain, psychiatric disorders  
 CC including depression and schizophrenia, neurodegenerative disease  
 CC including Alzheimer's, stroke and head trauma and neurological disorders  
 CC including migraine and epilepsy. The present sequence is human h-TRAAK-1  
 CC cDNA sequence #1  
 XX SQ Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3,44e-84 Length: 1182  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 3 Gaps: 2

US-09-655-272-2 (1-398) x AAA27105 (1-1182)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuValLeuValSerGly 20  
 DB 1 ATCGGACGACACACGCTCTCGGCCCTGCTGGCGCTGCTTGTCTTACTTGTGTCGT 60  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 DB 61 GCCCTGTGTTCGGGCGCCCTGGAGAGCCGCCACGAGCAGCAGCCGAGAGGAGCTGGGG 120  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 DB 121 GAGGTCCGAGAGAAGTTCTCTGAGGGCCCATCCGTGTGTGAGCGACCCAGGAGCTGGGCCTC 180  
 QY 61 PheIleIysLeuValGluAlaLeuGlyGlyGlyValAlaAsnProGluThrSerTrpThr 80  
 DB 181 CTATCAAGAGGTGGCTGATGCCCTGGGGAGGGGTGCGGACCCAGAACCAACTCGACC 240  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 241 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGAGCGCCTTCTTTCTCAGGGACC 297  
 QY 101 IleIleThrThrIleGlyThrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 298 ATCATCACCACCATCGCTATGCAATGTGGCCCTGCGCACAGATGCGGGCGCCTCTTC 357  
 QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 DB 358 TGCATCTTTTATCGCTGGTGGGGATTCCTGCTGTTGGGATCTTACTGGCAGGGCTGGG 417  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 DB 418 GACCGGCTGGGCTCTCTCCCTGGCCATGGCATCGGTACATTCAGCCATCTTCTTGAG 477  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180

DB 478 TGGCAGCTGCCACCGGAGCTAGTAAGAGTGTGTGGCGATGCTTTCTGTGATCGGC 537  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyMetGluSerTrpSerLys 200  
 DB 538 TGCCTGCTCTTTGTCTCCTCAGGCCACGTTTCGTGTTCTATATGAGGACTGGAGCAAG 597  
 QY 201 LeuGluAlaIleTyPheValIleValThrLeuThrValGlyPheGlyAspTrpVal 220  
 DB 598 CTGGAGGCCATCTACTTGTTCATAGTACGCTTACCACCGTGGGCTTGGCGCATATGTG 657  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyGlnProLeuValTrpPheTrpIle 240  
 DB 658 GCGGGCGCGGACCCAGGAGGACTCCCGGCTATCAGCGCTGTGTGTTCTGGATC 717  
 QY 241 LeuPheGlyLeuAlaTyPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 DB 718 CTGCTCGGCTGGCTTACTTTCCTCAGTGTCTCACCACCATCGGAACCTGGCTGCGAGTA 777  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 DB 778 GTGTCCGCGGCACCTCGGCGAGAGATGGGCGGCTCAGCGCTCAGCTGCAGCTGGACT 837  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 DB 838 GGCACAGTCACAGCGCGCTGACCCAGCAGCGCGGCGCCGCCCGCCCGCGGAGAG 897  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
 DB 898 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 945  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 DB 946 AGGCCCGCATCCCTTCGCGCCCGCGAGAAGGCTCAGCGCCTTCCCGCGCCACGGCTCG 1005  
 QY 341 AlaLeuAspTyProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
 DB 1006 GCCTTGATTTATCCGAGCAGAACCTGGCTTCATCAGAGTCTTCGGATACGACGAGC 1065  
 QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380  
 DB 1066 GAGCGCGCTGCCCGCTGCGCGCGCGGAGAGGTGCGCGCGCCCAATCCCGCCAGG 1125  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 DB 1126 AAGCCCGTGGCGCGCGCGCGCGCGCGCGCGTCCCGGAGACAAAGGCGTGGCGGTG 1179

RESULT 3  
 AAH78636  
 ID AAH78636 standard; cDNA; 1182 BP.  
 XX AC AAH78636;  
 XX 10-DEC-2001 (first entry)  
 DE Human mechanically sensitive potassium channel hTRAAK cDNA.  
 XX Human; mechanically sensitive potassium channel; riluzole; TWICK;  
 KW polyunsaturated fatty acid; arachidonic acid; hTRAAK; chromosome 11q13;  
 KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;  
 KW hormone secretion; cardiac disease; vascular disease; ischemia;  
 KW nervous system disorder; endocrinal disease; muscle disease;  
 KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1. .1182  
 FT /tag= a  
 FT /product= "mechanically sensitive potassium channel  
 FT hTRAAK"  
 XX WO200168670-A2.  
 XX

PD 20-SEP-2001.  
 XX 14-MAR-2001; 2001WO-FR000758.  
 XX 14-MAR-2000; 2000FR-00003264.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Lazdunski M, Lesage F, Maingret F;  
 XX WPI; 2001-590037/66.  
 XX P-PSDB; AAG67777.  
 XX New mechanically sensitive potassium channel, useful for treating  
 XX cardiovascular diseases and in drug screening, is activated by  
 XX polyunsaturated fatty acids.  
 XX Claim 4; Page 32-33; 37pp; French.  
 XX The present sequence encodes a human mechanically sensitive potassium  
 XX channel which is activated by polyunsaturated fatty acids (particularly  
 XX arachidonic acid (AA)) and by riluzole. The polypeptide is designated  
 XX human TWICK-related AA-activated potassium channel (hTRAAK). The hTRAAK  
 XX gene is located on chromosome 11q3. hTRAAK is involved in regulation of  
 XX neuronal and muscle excitation, cardiac rhythm and secretion of hormones.  
 XX Cells that express hTRAAK, designated to screen for modulators of hTRAAK  
 XX activity. Such modulators are potentially useful for prevention or  
 XX treatment, in humans and animals, of: cardiac and/or vascular disease;  
 XX nervous system disorders associated with ischemia and anoxia; endocrinal  
 XX diseases associated with anomalous hormone secretion or muscle diseases;  
 XX and retinal diseases. Typical examples are epilepsy, cardiac arrhythmia  
 XX and neurodegeneration  
 XX Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3,44e-84 Length: 1182  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 4 Gaps: 2  
 US-09-655-272-2 (1-398) x AAH78636 (1-1182)  
 QY 1 MetArgSerThrThrLeuLeuAlaLeuAlaLeuValLeuLeuTyrLeuValSerGly 20  
 Db 1 ATGGCAGCACCACCGCTCTGGCCCTCTGGCGCTGGTCTTGTCTTATCTTGTGTCTGGT 60  
 QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
 Db 61 GCCCTGGTGTTCGGGCCCTCGAGCAGCCGCCACGAGCAGCGCCACGAGGAGCTGGGG 120  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 Db 121 GAGTCCGAGAGAAGTTCTGAGGGCCCATCGGTGTGTGAGCGACGAGGAGCTGGGCCTC 180  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTyrThr 80  
 Db 181 CTCATCAAGGAGGTGGTGTATGTCCTCGGGAGGGGTGGCGGCCACCAACTCGACC 240  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 Db 241 AGCAACAGCAGCAC--TCAGCCTGGACCTGGGCGGCGCTTCTTTCTTCAGGGACC 297  
 QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyValLeuPhe 120  
 Db 298 ATCATCACCACTCGCTATGGAATGTGGCCCTCGCCACGACATCGCGGGCGCTCTTC 357  
 QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 Db 358 TGCATCTTTTATGCGCTGGGTGGGATTCCTGCTTTGGGATCTCTACTGGCAGGGTGGG 417

QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 Db 418 GACCGGTGGCTCTCTCCCTGGCCATGCAATCGGTACATTAAGCCATCTTCTTGAAG 477  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
 Db 478 TGGCAGCTGCCACCGGAGCTAGTAAGAGTCTGTGGCGATGCTTTCTCTGTATCGGC 537  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTyrSerLys 200  
 Db 538 TGCCTGTCTTTGTCTTCACGCCACGTTCTGTCTGTATATGAGGACTGGAGCAAG 597  
 QY 201 LeuGluAlaIleTyrPheValIleValThrThrThrValGlyPheGlyAspTyrVal 220  
 Db 598 CTGGAGCCATCTACTTTGTATAGTACGCTTACCACTGGGCTTGGCGACTATGTG 657  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTyrPheTyrIle 240  
 Db 658 GCCGCGCGGACCCAGGCGAGACTCCCCCGCTATCAGCGCTGTGTGTGTCTGGATC 717  
 QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTyrPheLeuAla 260  
 Db 718 CTGCTGGCTGGCTTACTTTCGCTCAGTCTCACCACCATCGGAACCTGGCTCGAGTA 777  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTyrThr 280  
 Db 778 GTGTCGCGCGCACTCGGGCAGAGATGGCGGCTCAGCGCTCAGGCTGCAGCTGGACT 837  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 Db 838 GGCACAGTACAGCGCGCTGACCCAGCGAGCGCGCGCGCGCGCGCGCGCGAGAG 897  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaValValGluProAlaGly 320  
 Db 898 GAGCAGCCACTG-----CTGCTCTCAGCGCTGTCCAGCGCAGCCGCTGGGC 945  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340  
 Db 946 AGGCGCCGATCCCTTCGCCCCCGGAGAGGCTCAGCGCTTCCCGCCCGCGGCTCG 1005  
 QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheLeuAspGluSerSerAspThrGlnSer 360  
 Db 1006 GCCTTGATATCCAGCGAGAACCTCGCTTCATCGACGAGTCTCTCGGATACGAGAGC 1065  
 QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgGlyArgProAsnProSerLys 380  
 Db 1066 GAGCGCGCTGCGCGCTGCGCGCGCGCGAGAGTCTCGCGCGCGCGCGCGCGCGAGG 1125  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 Db 1126 AGCCCGTGGCGGTG 1179  
 RESULT 4  
 AAA27106  
 ID AAA27106 standard; cDNA; 1218 BP.  
 XX  
 AC AAA27106;  
 XX  
 DT 04-AUG-2000 (first entry)  
 XX  
 DE Human h-TRAAK cDNA sequence #2.  
 XX  
 KW Human; h-TRAAK; potassium channel polypeptide;  
 KW 2P domain potassium channel; neurodegenerative disease; stroke;  
 KW psychiatric disorder; neurological disorder; Gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 37..1218  
 FT /\*tag= a  
 FT /product= "h-TRAAK protein #2"  
 XX

PN WO200026253-A1.  
 XX 11-MAY-2000.  
 XX 03-NOV-1999; 99WO-GB003634.  
 XX 03-NOV-1998; 98GB-00024048.  
 PR 07-OCT-1999; 99GB-00023668.  
 XX (SMIK ) SMITHLINE BERCHAM PLC.  
 XX Chapman CG, Duckworth DM;  
 XX WPI; 2000-365583/31.  
 DR P-PSDB; AAY94426.  
 XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of h-TRAAK  
 PT related disorders, e.g. depression and schizophrenia.  
 XX Claim 11; Page 21 and 22; 35pp; English.  
 XX Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK  
 CC polynucleotides from human tissue samples. h-TRAAK polypeptides have  
 CC homology to the 2P domain potassium channel family of polypeptides. The h  
 CC -TRAAK polypeptides and polynucleotides may be used in diagnostic assays  
 CC for conditions related to h-TRAAK imbalance and for identifying agonists  
 CC and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and  
 CC polynucleotides may also be useful for treatment and prevention (e.g. as  
 CC vaccines) of certain diseases, such as pain, psychiatric disorders  
 CC including depression and schizophrenia, neurodegenerative disease  
 CC including Alzheimer's, stroke and head trauma and neurological disorders  
 CC including migraine and epilepsy. The present sequence is human h-TRAAK  
 CC cDNA sequence #2  
 XX Sequence 1218 BP; 182 A; 421 C; 395 G; 220 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 3,546-84 Length: 1218  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 3 Gaps: 2

US-09-655-272-2 (1-398) x AAA27106 (1-1218)  
 QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20  
 DB 37 ATGCGCAGCACCACGCTCTGGCCCTGCTGGCGCTGCTTGTCTTGTCTGTCTGT 96  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40  
 DB 97 GCCTGTGTTCGGGCGCTTGGAGCAGCCACACAGCAGCAGCCACAGGAGCTGGGG 156  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 DB 157 GAGGTCGAGAGAAGTTCCTGAGGGCCCATCCGTGTGTGAGCAGCAGGAGCTGGCCCTC 216  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
 DB 217 CTCATCAAGGAGGTGCTGATGCCCTGGGAGGGGGTGGCAGCCACGAAACCACTCGACC 276  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 277 AGCAACAGCGCCAC---TCAGCCTGGACCTGGCAGCGCCCTCTTTCTCAGGGACC 333  
 QY 101 IleIleThrThrIleGlyTyrGlyValAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 334 ATCATCACCACCATCGCTATGCAATGTGGCCCTGGCAGACAGATGCCGGGCGCTCTTC 393  
 QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140

Db 394 TGCATCTTTATGCGCTGTGGGATTCGCTGTTTGGGATCTACTGCGAGGGGTGCGG 453  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGlyAlaIlePheLeuLys 160  
 Db 454 GACCGGCTGGGCTCCTCCCTGCGCCATGCGATCGGTACATTTGAAGCCATCTTTGAAG 513  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
 Db 514 TGGCAGTGCACCGGAGCTAGTAAGAGTGTGTGCGCGATGCTTTCTGCTGATCGGC 573  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 Db 574 TGCCTGCTCTTTGTCTCAGCCACGTTCTGTTCTGTATATGAGGACTGAGACGAG 633  
 QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220  
 Db 634 CTGGAGGCCATCTACTTTGTATAGTACGCTTACCACGTTGGGCTTTGGCGACTATGTG 693  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
 Db 694 GCGGCGCGGAGCCCGGAGGACTCCCGGCTATCAGCCGCTGTGTGTGTTCTGGATC 753  
 QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 Db 754 CTGCTCGGCTGGCTTACTTTCCTCAGTGTCTACACCATCGGAACTGGCTCGAGTA 813  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 Db 814 GTGTCCGCGCACCTCGGCGAGATGGCGGCTCAGGCTCAGGCTGCCAGCTGGACT 873  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 Db 874 GGCACAGTGCACGCGCGTGCACCGAGCGCGCGCGCGCGCGCGCGCGCGCGAGAG 933  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
 Db 934 GAGCAGCCACTG-----CTGCCCTCAGCCGCTGTCCAGCGCGCGCTGGGC 981  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 Db 982 AGGCCCGGATCCCTTCGCCCCCGAGAGGCTCAGCGGCTTCCCGCGCCAGCGCTCG 1041  
 QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerSerThrGlnSer 360  
 Db 1042 GGCCTGGATTATCCAGCGAGAACCTGGCTTTCATCGAGAGTCTCTCGGATACGAGAGC 1101  
 QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380  
 Db 1102 GAGCGGCTGCCGCTGCCCGCGCGGAGAGGTGCGCGCGCCCAATCCCCCAGG 1161  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 Db 1162 AGCCCGTGGCGCGCGCGCGCGCTCCCGAGACAAAGGCGTGGCGGTG 1215  
 RESULT 5  
 AAH99922  
 ID AAH99922 standard; cDNA; 1257 BP.  
 XX  
 AC AAH99922;  
 XX  
 DT 25-JAN-2002 (first entry)  
 XX  
 DE Nucleotide sequence of human TWIK-8 receptor channel.  
 XX Human; potassium channel; transmembrane domain: TWIK; TWIK-8;  
 KW Tandem of P domain in a Weak Inward rectifying K<sub>v</sub> channel; K<sub>v</sub>;  
 KW central nervous system disorder; cardiovascular disease;  
 KW potassium channel mediated disorder; Alzheimers disease;  
 KW Parkinsons disease; multiple sclerosis; Picks disease;  
 KW neurodegenerative disorder; Lewy diffuse body disease; senile dementia;  
 KW Huntingtons disease; movement disorder; epilepsy; AIDS related dementia;  
 KW Gilles de la Tourettes syndrome; amyotrophic lateral sclerosis;  
 KW progressive supranuclear palsy; Jakob-Creutzfeldt disease;

autonomic function disorder; neuropsychiatric disorder; phobia;  
 bipolar affective disorder; ss; nootropic; neuroprotective;  
 antiparkinsonian; antiarteriosclerotic; cyostatic; hypotensive;  
 antidepressant; antimigraine; analgesic; vasotropic; anticonvulsant;  
 neuroprotective; tranquilizer; neuroleptic; cancer;  
 learning and memory disorder; cell proliferation disorder.

Homo sapiens.

Key Location/Qualifiers  
 CDS 1. .1257  
 /tag= a  
 /product= "human TWIK-8"  
 /partial  
 /note= "No stop codon"

W020017329-A2.  
 18-OCT-2001.  
 06-APR-2001; 2001WO-US011301.  
 07-APR-2000; 2000US-0195734P.  
 (MILL-) MILLENIUM PHARM INC.  
 Gluckemann WA;  
 WPI; 2002-010911/01.  
 P-PSDB; AAG78406.

Novel isolated 12303, a human tandem of P domains in a weak inward  
 rectifying potassium channel-related potassium channel subunit  
 polypeptide useful for treating Alzheimer's disease, restenosis, migraine  
 and cancer.

Claim 1; Page 122-124; 124pp; English.

This invention relates to a human TWIK-8 (tandem of P domains in a weak  
 inward rectifying K<sup>+</sup> channel)-related potassium channel subunit  
 polypeptide. Applications of the polypeptide include: nootropic,  
 neuroprotective, antiparkinsonian, antiarteriosclerotic, cyostatic,  
 hypotensive, antidepressant, antimigraine, analgesic, vasotropic,  
 anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene  
 therapy, and as a modulator of potassium channel mediated activity in a  
 cell, and is useful in screening assays, detection assays, predictive  
 medicine and in methods of treatment. The polypeptide is useful as a  
 target for developing modulating agents to regulate a variety of cellular  
 processes, and is also useful as query sequence to perform a search  
 against public databases to, for example, identify other family members  
 or related sequences. The polypeptide is useful for treating disorders  
 characterized by insufficient or excessive production of TWIK-8 protein  
 or production of TWIK-8 protein forms which have decreased, aberrant or  
 unwanted activity compared to TWIK-8 wild type protein, e.g., potassium  
 channel associated disorders including central nervous system disorders  
 such as cognitive and neurodegenerative disorders, autonomic function  
 disorders, learning or memory disorders, cardiac disorders, muscular  
 disorders, pain disorders and disorders of cellular growth,  
 differentiation or migration. The polypeptide is useful as immunogen to  
 raise anti-TWIK-8 antibodies, and to screen for drugs, and is also  
 considered useful for producing non-human transgenic animals. This  
 sequence represents the nucleotide sequence for human TWIK-8, which  
 differs to the sequence in AAH99922 since it does not contain the 3',  
 untranslated region

Sequence 1257 BP; 188 A; 443 C; 404 G; 222 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3.66e-84 Length: 1257  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5

DB: 6 Gaps: 2  
 US-09-655-272-2 (1-398) x AAH99922 (1-1257)  
 QY 1 MetArgSerThrThrLeuAlaLeuAlaLeuValLeuLeuValSerGly 20  
 DB 79 ATGGCAGACACACGCTCTGGCCCTGCTGGCGCTGGTCTTGTCTTACTTGGTCTGGT 138  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
 DB 139 GCCCTGGTGTTCGGGGCCCTGGAGCAGCCCCACGAGCAGAGGAGGAGGAGGAGG 198  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 DB 199 GAGGTCCGAGAGAAATTCCTGAGGGCCCATCCGTGTGTGAGCGACCGAGGAGCTGGGCTC 258  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
 DB 259 CTCATCAAGGAGGTGGTGTATGCCCTGGAGGGGTGGGACCCAGAAACCACTCGACC 318  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 DB 319 AGCAACACAGCCAC-TCAGCCTGGACCTGGCGACGCGCTTCTTTTCTCGAGGACC 375  
 QY 101 IleIleThrIleGlyTyGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 DB 376 ATCATCACCCATCGGCTATGGCAATGTGGCCCTGGCAGCAGATGCCGGCGCTCTTC 435  
 QY 121 CysIlePheTyAlaLeuValGlyIleProLeuPheGlyMetLeuAlaGlyValGly 140  
 DB 436 TGCATCTTTATGCGCTGGTGGGATTCGGCTGTTGGGATCTTACTGCGAGGGGTGGG 495  
 QY 141 AspArgLeuSerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 DB 496 GACCGCTGGGCTCCTCCCTGGCCATGGCATCGGTCTCATTTGAAGCCATCTTCTTGAG 555  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
 DB 556 TGGCAGTGGCCACCGAGCTAGTAAGAGTGTGTCGGGATGCTTTTCTGCTGATCGG 615  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 DB 616 TGCCTGCTTTTGTCTCAGGCCACGTCGTGTGTCTGTATATATGAGGACTTGGAGCAAG 675  
 QY 201 LeuGluAlaIleTyPheValIleValThrLeuThrValGlyPheGlyAspTyVal 220  
 DB 676 CTGGAGGCCATCTACTTTGTCTAGTACGCTTACCGCGTGGGCTTTGGCGACTATGTG 735  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyGlnProLeuValTrpPheTrpIle 240  
 DB 736 GCGGGCGGGACCCCGAGGAGGACTCCCGGCTATCAGCCGCTGGTGTGGTCTTGGATC 795  
 QY 241 LeuPheGlyLeuAlaTyPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 DB 796 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCCATCGGAACTGGGCTGGAGTA 855  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 DB 856 GTGTCCCGGCACTCGGCGAGATGGCGGCGCTCACGGCTCAGGCTCCAGCTGGGCTG 915  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 DB 916 GGCACAGTGCACGCGCGTGCACCCAGCGCGGCGCGCGCGCGCGCGCGCGGAGAAG 975  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320  
 DB 976 GAGCAGCCACTG-----CTGCCCTCCACCGCCCTGTCCAGCGCAGCGCGCTGGGC 1023  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 DB 1024 AGGCCCGGATCCCTTCGCCCCCGGAGAGGCTCAGCCGCTTCCCGGCCACCGGCTCG 1083  
 QY 341 AlaLeuAspTyProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360

Db 1084 GCCTGGATTATCCAGCGAGACCTGGCCCTTCATCGACGAGTCTCGGTATCCGAGC 1143  
 QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProSerLys 380  
 Db 1144 GAGCGGGCTGCGCGTGGCCCGCGCGAGAGGTGCGCGCCGCGCCAAATCCCCAGG 1203  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 Db 1204 AAGCCCGTGGCG 1257  
 RESULT 6  
 ADI27937  
 ID ADI27937 standard; cDNA; 1257 BP.  
 XX  
 AC ADI27937;  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human TWIK-8 cDNA coding region.  
 XX  
 KW Human; TWIK-8; gene; ss; ion channel family; ICF; cancer; leukaemia;  
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;  
 KW hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;  
 KW nootropic; antiparkinsonian; hepatotropic; cardiovascular.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003165891-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 15-MAY-2002; 2002US-00146733.  
 XX  
 PR 29-FEB-2000; 2000US-00515520.  
 PR 29-FEB-2000; 2000US-0185388P.  
 PR 03-MAR-2000; 2000US-00518866.  
 PR 07-APR-2000; 2000US-0195734P.  
 PR 11-APR-2000; 2000US-0195993P.  
 PR 26-APR-2000; 2000US-0199799P.  
 PR 19-SEP-2000; 2000US-0233537P.  
 PR 25-SEP-2000; 2000US-0235018P.  
 PR 25-SEP-2000; 2000US-0235059P.  
 PR 15-DEC-2000; 2000US-0256240P.  
 PR 18-DEC-2000; 2000US-0256588P.  
 PR 21-DEC-2000; 2000US-0258028P.  
 PR 28-FEB-2001; 2001US-00796720.  
 PR 06-APR-2001; 2001US-00828035.  
 PR 11-APR-2001; 2001US-00833081.  
 PR 25-APR-2001; 2001US-00843128.  
 PR 19-SEP-2001; 2001US-00957683.  
 PR 25-SEP-2001; 2001US-00964252.  
 PR 25-SEP-2001; 2001US-00964256.  
 PR 17-DEC-2001; 2001US-00024623.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Curtis RAJ, Glucksmann MA, Silos-Santiago I;  
 XX  
 DR P-PSDB; ADI27936.  
 DR  
 DR WPI; 2004-069000/07.  
 XX  
 XX P-PSDB; ADI27936.  
 XX  
 PT TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,  
 PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for  
 PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and  
 PT cardiovascular disorders.  
 XX  
 PS Claim 1; SEQ ID NO 30; 638pp; English.  
 XX  
 PS The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,  
 CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel  
 CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,  
 CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC 53763 ICF nucleic acids and proteins may be used for preventing,  
 CC diagnosing and treating ICF-related diseases. The sequences may be used  
 CC to treat disorders associated with decreased expression by rectifying  
 CC mutations or deletions in a patient's genome that affect the activity of  
 CC ICF proteins by expressing inactive proteins or to supplement the  
 CC patients own production of ICF proteins. The proteins may also be used as  
 CC antigens in the production of antibodies against ICF proteins and in  
 CC assays to identify modulators of ICF protein expression and activity. The  
 CC anti-ICF protein antibodies, agonists and antagonists may be used to  
 CC regulate ICF protein expression and activity. The antibodies may also be  
 CC used as diagnostic agents for detecting the presence of ICF proteins in  
 CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used  
 CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers  
 CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple  
 CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This  
 CC sequence represents cDNA encoding the human TWIK-8 protein of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 SQ Sequence 1257 BP; 188 A; 443 C; 404 G; 222 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3-66e-84 Length: 1257  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 12 Gaps: 2  
 US-09-655-272-2 (1-398) x ADI27937 (1-1257)  
 QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuLeuLeuValSerGly 20  
 Db 79 ATGCGCAGCACCACCGCTCCTGCGCCCTGCTGGCGCTGCTTGTCTTGTCTGTCTGT 138  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
 Db 139 GGCCTGTGTCTTCCGGCCCTTGGAGCAGCCCGCAGCAGCAGCGGAGGAGCTGGGG 198  
 QY 41 HisGlyArgAspGlnPheLeuArgPheHisProCysValSerGlnLysSerLeuGluAsp 60  
 Db 199 GAGTCCGAGAGAGAGTCTCTGAGGGCCCATCGGTGTGTGAGCAGCAGGAGCTGGGCC 258  
 QY 61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
 Db 259 CTCATCAAGAGGTGGTGTGATGCTTGGAGGGGTGCGGACCCAGAAACCAACTCGACC 318  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 Db 319 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGCGAGCGCTCTTTTCTCAGGGACC 375  
 QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 Db 376 ATCATCACCAACCATCGGCTATGGCAATGTGGCCCTGCGCAGCAGATCGCGGCGCTTTC 435  
 QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 Db 436 TGCATCTTTTATGCGCTGTGGTGATTCGCTGTTTGGGATCCTACTGGCAGGGCTCGGG 495  
 QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 Db 496 GACCGGCTGGGCTCTCCCTCGCCCATGGCATGGGTGCGGTCACATTGAAGCCATCTTCTTGAAG 555  
 QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
 Db 556 TGCACGTGCCACCGAGGTAGTAAGAGTGTGTGCGGATGCTTCTTCTGTCATCGGC 615  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 Db 616 TGCCTGTCTTGTCTCTCACGCCCGCTTGTGTTCTGTCTATATGAGGAGCTGGAGCAAG 675  
 QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220

Db 676 CTGAGGCCATCTACTTTGTCTATAGTACGCTTACCACCGTGGCTTTGGCGACTATGTG 735  
 QY 221 ProGlyAspGlyThrGlyGlnAenSerProAlaTyxGlnProLeuValTrpPheTrpIle 240  
 Db 736 GCCGGGGCGGACCCAGGAGGACTCCCGGCTATACAGCGCTGTGTGTTCTGGATC 795  
 QY 241 LeuPheGlyLeuAlaTyxPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 Db 796 CTGCTCGGCTGGCTTACTTGGCTCAGTGCTCACCACCATCGGAACCTGGCTCGGAGTA 855  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 Db 856 GTGTCGCGCGCATCTGGGCGAGATGGCGGCTCACGCTCAGCTGCCAGCTGGACT 915  
 QY 281 GlyThrValThrAlaArgValThrGlnAtrThrGlyProSerAlaProProGluLys 300  
 Db 916 GGCACAGTGACAGGCGGTGATCCAGCGAGCGCGGCGCGCGCGCGCGCGCGGAGAG 975  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
 Db 976 GAGCAGCCACTG-----CTGCTCTCACCGCGCTGTCTCAGCGCAGCGCTGGGC 1023  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 Db 1024 AGGCCCGGATCCCTTGGCCCTCCGAGAGGCTCAGCGCGCTTCCCGCCACGCGCTCG 1083  
 QY 341 AlaLeuAspTyxProSerGluAenLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
 Db 1084 GCCTGTGATATCCAGCGAGAACCTTGGCTTTCATCGACGATCTCTCGATAGCGAGAGC 1143  
 QY 361 GluArgGlyCysAlaLeuProAlaProAlaProAlaProAlaProAlaProAlaProAla 380  
 Db 1144 GAGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 Db 1204 AAGCCCGTGGCGGTG 1257  
 RESULT 7  
 ID ADH51640 standard; DNA; 1260 BP.  
 XX AC ADH51640;  
 XX DT 25-MAR-2004 (first entry)  
 XX DE Human 12303 protein coding DNA sequence.  
 KW cytotatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;  
 KW respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;  
 KW immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;  
 KW antianaemic; endocrine-Gen; neuroprotective; notropic; cardiatic;  
 KW gene therapy; cellular proliferative; differentiative disorder; brain;  
 KW blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;  
 KW pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;  
 KW immune disorder; inflammatory disorder; cardiovascular disorder;  
 KW endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesis;  
 KW neoplastic; endocrine disorder; neurological; heart; tissue typing;  
 KW chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;  
 KW ds; 12303.  
 OS Homo sapiens.  
 XX PN US2003219806-A1.  
 XX PD 27-NOV-2003.  
 XX PF 18-MAR-2003; 2003US-00391399.  
 XX PR 22-FEB-2000; 2000US-00510706.  
 PR 07-APR-2000; 2000US-0395734P.  
 PR 31-MAY-2000; 2000US-00583373.  
 PR 26-JUN-2000; 2000US-0214176P.

08-AUG-2000; 2000US-00634669.  
 31-AUG-2000; 2000US-0229036P.  
 19-SEP-2000; 2000US-0233537P.  
 01-FEB-2001; 2001US-0267076P.  
 20-FEB-2001; 2001US-00789481.  
 12-MAR-2001; 2001US-0275078P.  
 12-MAR-2001; 2001US-0275172P.  
 06-APR-2001; 2001US-0082803S.  
 26-JUN-2001; 2001US-00891762.  
 29-AUG-2001; 2001US-00942447.  
 17-SEP-2001; 2001US-0322983P.  
 19-SEP-2001; 2001US-0095768S.  
 27-SEP-2001; 2001US-0325854P.  
 04-DEC-2001; 2001US-0336936P.  
 31-JAN-2002; 2002US-00062937.  
 08-MAR-2002; 2002US-00094214.  
 11-MAR-2002; 2002US-00095139.  
 17-SEP-2002; 2002US-00245121.  
 26-SEP-2002; 2002US-00255532.  
 04-DEC-2002; 2002US-00309804.  
 (MILL-) MILLENNIUM PHARM INC.  
 Glucksmann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;  
 WPI; 2004-010868/01.  
 P-PSDB; ADH51639.  
 XX New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,  
 55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,  
 useful for diagnosing, preventing or treating e.g. proliferative or brain  
 disorders.  
 XX Claim 1; SEQ ID NO 20; 276pp; English.  
 XX This invention relates to novel human DNA sequences (designated 18607,  
 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,  
 52991, 59914, 59921 or 33751) and the proteins encoded by them. The  
 invention may be useful for the development of compounds with a  
 cytotatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen,  
 respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,  
 immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic,  
 antianaemic, endocrine-Gen, neuroprotective, notropic or cardiatic  
 activity. In addition, the sequences may be useful for gene therapy. The  
 invention may be useful in diagnosing, preventing or treating disorders  
 characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433,  
 38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for  
 example cellular proliferative and/or differentiative disorder, brain  
 disorder, blood vessel disorder, platelet disorder, breast disorder,  
 colon disorder, kidney disorder, lung disorder, ovarian disorder,  
 prostate disorder, pancreatic disorder, skeletal muscle disorder,  
 testicular disorder, hormonal disorder, disorder associated with bone  
 metabolism, immune disorder, inflammatory disorder, cardiovascular  
 disorder, endothelial cell disorder, liver disorder, viral disease, pain,  
 metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder,  
 endocrine disorder, neurological disorder or heart disorder. They may  
 also be used in screening assays, tissue typing, chromosomal mapping,  
 CC predictive medicine or pharmacogenomics. The present sequence is that of  
 the coding DNA sequence for the human 12303 protein of the invention.  
 XX SQ Sequence 1260 BP; 189 A; 443 C; 405 G; 223 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3,67e-84 Length: 1260  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 DB: 12 Gaps: 2

US-09-655-272-2 (1-398) x ADH51640 (1-1260)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuValSerGly 20

Db 79 ATGCGAGCACCAGCTTCTGGCCCTGCTGCGCTGCTTGTACTTGGTGTCTGGT 138  
Qy 21 AlaleuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40  
Db 139 GCCTGGTGTTCGGGCGCTGGAGCAGCCACAGCAGCAGCAGCAGGAGAGCTGGG 198  
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
Db 199 GAGGTCCGAGAGAAGTCTCTGAGGGGCCATCCGTGTGTGAGCAGCAGGAGCTGGGCTC 258  
Qy 61 PheIleIysLeuValGluAlaLeuGlyValGlyAlaAsnProGluThrSerTrpThr 80  
Db 259 CTATCAAGGAGGTGGTGATGCCCTGGAGGGGGTGGAGCCAGAACCACTCGACC 318  
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
Db 319 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGCAGCGCCTCTTTTCTCAGGGACC 375  
Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
Db 376 ATCATCACCACTCGCTATGCAATGTGGCCTCGCACAGATCGCGGCGCTCTTC 435  
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db 436 TGATCTTTTATGCTGTGGTGGGATTCGCTGTTGGGATCTTACTGGCAGGGTGGG 495  
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db 496 GACCGGTGGCTCTCTCCCTGCGCATGGATGGTCACATTCAGCCATCTTCGAG 555  
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
Db 556 TGGCAGCTGCCACCGAGCTAGTAAGAGTGTCTGCGCGATGCTTTTCTGCTGATCGGC 615  
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
Db 616 TGCTGTCTCTTGTCTCACGCCCGCATGCTGTCTTCTATATGAGGAGCTGGAGCAAG 675  
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220  
Db 676 CTGGAGCCATCTACTTGTCTATGATGACGCTTACACCGTGGCTTTGGCGACTATGTG 735  
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
Db 736 GCCGGCGCGACCCAGCAGGACTCCCGGCTATCAGCGCTGTGTGTCTGATC 795  
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
Db 796 CTGCTCGGCTGGCTTACTTCTGCTCTAGTGTCTCACCACCATCGGAACTGGCTGGAGTA 855  
Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
Db 856 GTGTCCCGCCGCACTCGGCGAGATGGGGGCTCAGGCTCAGGCTCAGCTGGACT 915  
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
Db 916 GGCACAGTACAGCGCGTGTACCCAGCAGCGCGGCGCGCGCGCGCGCGGAGAG 975  
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValGluProAlaGly 320  
Db 976 GAGCAGCCACTG-----TGCTCTCCAGCCGCTGTCCAGCGCAGCGCGCTGGGC 1023  
Qy 321 ArgProGlySerProAlaProAlaGluValGluThrProSerProProThrAlaSer 340  
Db 1024 AGGCCCGCATCTCTCCCGCCCGGAGAGCTCAGCGGCTTCCCGCCCGCAGGCTCG 1083  
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
Db 1084 GCCTGGATTATCCAGCAGAGAACCTGGCTTCATCGACAGTCTTCGGATACGACAGC 1143  
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380  
:::

Db 1144 GAGCGCGGCTGCCGCTGCCCGCGCGCGAGAGTCCGCGCCCAATCCCCCAGG 1203  
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
Db 1204 AAGCCGTCGCGCGCGCGCGCGCGCGCTCCCCGAGACAAAGGCGTGGCGGTG 1257  
RESULT 8  
AAH99921  
ID AAH99921 standard; cDNA; 1408 BP.  
XX AAH99921;  
AC  
XX 25-JAN-2002 (first entry)  
DT  
DE Nucleotide sequence of human TWIK-8 receptor channel.  
XX  
XX Human; potassium channel; transmembrane domain; TWIK; TWIK-8;  
KW Tandem of P domain in a Weak Inward rectifying K+ channel; K+;  
KW central nervous system disorder; cardiovascular disease;  
KW potassium channel mediated disorder; Alzheimers disease;  
KW Parkinsons disease; multiple sclerosis; Picks disease;  
KW neurodegenerative disorder; Lewy diffuse body disease;  
KW Huntingtons disease; movement disorder; epilepsy; AIDS related dementia;  
KW Gilles de la Tourettes syndrome; amyotrophic lateral sclerosis;  
KW progressive supranuclear palsy; Jakob-Creutzfeldt disease;  
KW autonomic function disorder; ss; nontropic; neuroprotective;  
KW bipolar affective disorder; ss; nontropic; neuroprotective;  
KW antiparkinsonian; antiarteriosclerotic; cyostatic; hypotensive;  
KW antidepressant; antimigraine; analgesic; vasotropic; anticonvulsant;  
KW neuroprotective; tranquilizer; neuroleptic; cancer;  
KW learning and memory disorder; cell proliferation disorder.  
XX  
OS Homo sapiens.  
FH  
FT Key Location/Qualifiers  
FT CDS 84..1343  
FT /\*tag= a /product= "human TWIK-8"  
FT  
XX W0200177329-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX  
PF 06-APR-2001; 2001WO-US011301.  
XX  
PR 07-APR-2000; 2000US-0195734P.  
XX  
XX (MILL-) MILLENIUM PHARM INC.  
PA Glucksmann MA;  
XX  
XX WPI; 2002-010911/01.  
PI P-PSDB; AAG78406.  
XX  
XX Novel isolated 12303, a human tandem of P domains in a weak inward  
PT rectifying potassium channel-related potassium channel subunit  
PT polypeptide useful for treating Alzheimer's disease, restenosis, migraine  
PT and cancer.  
XX  
XX Claim 1; Fig 1; 124pp; English.  
PS  
XX  
XX This invention relates to a human TWIK-8 (tandem of P domains in a weak  
CC inward rectifying K+ channel)-related potassium channel subunit  
CC polypeptide. Applications of the polypeptide include: nontropic,  
CC neuroprotective, antiparkinsonian, antiarteriosclerotic, cyostatic,  
CC hypotensive, antidepressant, antimigraine, analgesic, vasotropic,  
CC anticonvulsant, neuroprotective, tranquilizer, neuroleptic, in gene  
CC therapy, and as a modulator of potassium channel mediated activity in a  
CC cell, and is useful in screening assays, detection assays, predictive  
CC medicine and in methods of treatment. The polypeptide is useful as a  
CC target for developing modulating agents to regulate a variety of cellular  
CC processes, and is also useful as query sequence to perform a search  
CC against public databases to, for example, identify other family members



or related sequences. The polypeptide is useful for treating disorders characterized by insufficient or excessive production of TWIK-8 protein or production of TWIK-8 protein forms which have decreased, aberrant or unwanted activity compared to TWIK-8 wild type protein, e.g., potassium channel associated disorders including central nervous system disorders such as cognitive and neurodegenerative disorders, autonomic function disorders, learning or memory disorders, cardiac disorders, muscular disorders, pain disorders and disorders of cellular growth, differentiation or migration. The polypeptide is useful as immunogen to raise anti-TWIK-8 antibodies, and to screen for drugs, and is also considered useful for producing non-human transgenic animals. This sequence represents the nucleotide sequence for human TWIK-8.

SQ Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4.12e-84 Length: 1408  
 Score: 1692.50 Matches: 328  
 Percent Similarity: 88.44% Conservative: 24  
 Best Local Similarity: 82.41% Mismatches: 41  
 Query Match: 81.41% Indels: 5  
 Gaps: 2

US-09-655-272-2 (1-398) x AAH99921 (1-1408)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuValSerGly 20  
 Db 162 ATGCCAGACACAGCTCTGGCCCTGCTGGCTGTCTTACTTGTGTCTGT 221  
 QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
 Db 222 GCCCTGTGTTCGGGCGCTGGAGCAGCCACAGCAGCAGCAGCAGGAGGAGG 281  
 QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
 Db 282 GAGTCCGAGAGAGAGTTCCTGAGGCGCCATCCGCTGTGAGCCAGCAGGAGCTGGGCTC 341  
 QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaLeuGlyAlaLeuGlyAlaLeuGly 401  
 Db 342 CTCATCAAGGAGGTGGTGATCCCTGGAGGGGTGGGAGCCAGAACCAACTCGACC 401  
 QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
 Db 402 AGCAACAGCAGCCAC---TCAGCCTGGGAGCTGGGAGCCCTCTCTTTCTCAGGGACC 458  
 QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
 Db 459 ATCATCACCACTCGGCTATGGCAATGTGCCCTGGCAGCAGATGCGGGCGGCTCTTC 518  
 QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
 Db 519 TGCATCTTTATGCTGTGGGATTCGCTGTTGGATCCTTACTGGCAGGGGTGGG 578  
 QY 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
 Db 579 GACCGGTGGGCTCTCCCTCGGCATGGCATCGCTCACATTTGAAGCCATCTTCTTGAAG 638  
 QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
 Db 639 TGGCAGGTGGCCAGCAGCTAGTAAGAGTGTGTGGGATGCTTTCTTCTGTGATCGGC 698  
 QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
 Db 699 TGCCTGCTCTTTGCTCTCACGCCAGCTGCTGTTCTGTATATGGAGGAGTGGAGCAAG 758  
 QY 201 LeuGluAlaIleTyrPheValIleValThrThrThrValGlyPheGlyAspTyrVal 220  
 Db 759 CTGGAGGCACTACTATTTGTATAGTACGCTTACACCGTGGGCTTTGGCGCATATGTG 818  
 QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
 Db 819 GCCGGCGGGACCCAGCAGGACTCCCGCGCCTATCAGCGGCTGTGTGTTCTGGATC 878

QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
 Db 879 CTGCTCGGCTGGCTTACTTGGCTTCTAGTGTTCACCACTGGGAATCGGCTGGAGTA 938  
 QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
 Db 939 GTGTCCCGCGCACCTCGGCGAGATGGCGGCTTACGGCTCAGGCTGCCAGCTGGACT 998  
 QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
 Db 999 GGCACAGTGACAGCGGCTGTACCCAGCAGCGCGCGCGCGCGCGCGCGCGGAGAAG 1058  
 QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
 Db 1059 GAGCAGCCACTG-----CTGCTCCACCGGCTTCTCCAGCAGCGCGCTGGGC 1106  
 QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
 Db 1107 AGGCCCCGATCCCTTGCCTCCCGAGAGGCTCAGCGCTTCCCGCCACGCGCTCG 1166  
 QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
 Db 1167 GCCTGGATTATCCAGCGAGAACCTGGCTTCTATCGACGAGTCTCTCGGATACGAGAGC 1226  
 QY 361 GluArgGlyCysAlaIleuProAlaProAlaProArgGlyArgArgProAsnProSerLys 380  
 Db 1227 GAGCGCGGTGCTGCGCTGCGCGCGCGCGAGAGTCCCGCGCCCAATCCCCCAGG 1286  
 QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
 Db 1287 AAGCCGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 1340  
 RESULT 9  
 ID ADK52549 standard; DNA; 1408 BP.  
 XX ADK52549;  
 DT 06-MAY-2004 (first entry)  
 XX Hematological disorder associated Gene ID 12303.  
 DE  
 XX cytostatic; antianemic; antisickling; virucide; hemostatic; nephrotropic;  
 KW cytostatic; thrombolytic; antiparasitic; gene therapy;  
 KW hematologic disorder; cancer; Sickle Cell Anemia;  
 KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;  
 KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;  
 KW transfusion reaction; Erythroblastosis; mechanical trauma;  
 KW micro-angiopathic hemolytic anemia; parasite infection; gene; ds.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 PH 84..1343  
 FT CDS /\*tag= a  
 FT WO2003065871-A2.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 28-JAN-2003; 2003WO-US002484.  
 XX  
 PR 04-FEB-2002; 2002US-0354333P.  
 PR 28-FEB-2002; 2002US-0360258P.  
 PR 15-MAR-2002; 2002US-0364476P.  
 PR 26-APR-2002; 2002US-0375626P.  
 PR 06-JUN-2002; 2002US-0386494P.  
 PR 24-JUN-2002; 2002US-0390965P.  
 PR 28-JUN-2002; 2002US-0392480P.  
 PR 03-JUL-2002; 2002US-0394128P.  
 PR 31-JUL-2002; 2002US-0399783P.  
 PR 13-AUG-2002; 2002US-0403221P.  
 PR 30-AUG-2002; 2002US-0407045P.



25-NOV-2002; 2002US-0429048P.  
(MILL-) MILLENNIUM PHARM INC.  
Carroll JM, Healy A, Weich NS, Kelly LM;  
WPI; 2003-731464/69.  
P-PSDB; ADK52550.  
Identifying a compound capable of treating a hematologic disorder (e.g. anemia or leukemia) comprises assaying the ability of the compound to modulate the expression or activity of e.g. 131,148, 199 or 12303 polypeptide or nucleic acid.  
Disclosure; SEQ ID NO 7; 232pp; English.  
The invention relates to a method of identifying a compound capable of treating a hematologic disorder comprises assaying the ability of the compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic acid expression or polypeptide activity, thus, identifying a compound capable of treating a hematologic disorder. The methods are useful in diagnosing, preventing and treating hematological disorders, such as cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia, Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders associated with an increased risk of Thrombosis, Herpes, Thalassemia, antibody-mediated disorders such as transfusion reactions and Erythroblastosis, mechanical trauma to red blood cells such as microangiopathic hemolytic anemias, infections by parasites or chemical injuries. The methods may also be used for identifying compounds that modulate hematological disorders. This sequence corresponds to one of the genes modulated the compound.  
Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other

Alignment Scores:	
Pred. No.:	4, 12s-84
Score:	1692.50
Percent Similarity:	88.44%
Best Local Similarity:	82.41%
Query Match:	81.41%
DB:	10
	10
	5
	Indels:
	41
	Mismatches:
	24
	Conservative:
	328
	Matches:
	1408

US-09-655-272-2 (1-398) x ADK52549 (1-1408)

Qy	1	MetArgSerThr	LeuLeuAlaLeuValLeuTyrLeuValSerGly	20
Db	162	ATGCGCAGCACCA	CGCTCGGCCCTGTCGGCTGGTCTTGCTTTATCTGGTGTCTGGT	221
Qy	21	AlaLeuValPheGln	AlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp	40
Db	222	GCCTCGGTGTC	CGGCGCCCTGAGCAGGCCCCACGACGACGAGCGAGGAGCTGGGG	281
Qy	41	HisGlyArgAspGln	PheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp	60
Db	282	GAGGTCCGAGAG	AGTTCTCTGAGGCCCATCCGTGTGTGAGCGACGAGGAGCTGGGCCCTC	341
Qy	61	PheLeuLysLeuVal	GluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr	80
Db	342	CTCATCAAGAGGT	GGTCTCCCTGGGAGGGGGTGGGACCCAGAAAAACAATCTGCACC	401
Qy	81	AsnSerSerAsnHis	SerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr	100
Db	402	AGCAACAGCAGG	CCAC---TCAGCCTGGGACCTGGGACGCGCTTCCTTTTCTCAGGGACC	458
Qy	101	IleIleThrThr	IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe	120
Db	459	AATCATCACCAC	CATCGGCTATGGCAATGTGGCCCTGCCACAGATGCGGGCGGCTCTTC	518
Qy	121	CysIlePheTyrAla	LeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly	140
Db	519	TGCATCTTTTAT	CGCTGGTGGGATCCGCTGTTGGATCCTACTGGCAGGGGTCTGGG	578

Qy	141	AspArgLeuGlySerSerLeuArgArgGlyLeGlyHisIleGluAlaIlePheLeuLys	160
Db	579	GACCGGCTGGGGCTCCTCCCTCGCCCATGGCATCGGTACATCAATGAAGCAATCTTCTTGAAG	638
Qy	161	TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuLeGly	180
Db	639	TGGCACGTGCCACCGGAGCTAGTAGAGTCTGTTCGGCGATGCTTTTCTCTGCTGATCGGC	698
Qy	181	CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys	200
Db	699	TGCCTGCTCTTTGCTCTACGCCACCGTTCGTCTGTCTGTATATGGAGGACTGGAGCAAG	758
Qy	201	LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal	220
Db	759	CTGAGGCCATCTACTTTGTTCATAGTAGACCTTACCACTGGGCTTTGGCGACTATGTG	818
Qy	221	ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle	240
Db	819	GCCGGCGGACCCAGGCAGGACTCCCCGGCTATCAGCCGCTGGTGTGTCTGGATC	878
Qy	241	LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla	260
Db	879	CTGCTCGCCCTGGCTACTTTCGCTCAGTCTCACCACCATCGGAACTCGCTGCGAGTA	938
Qy	261	ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr	280
Db	939	GTGTCCCGCCGACTCGGGCAGAGATGGCGGCTCTACGGCTCAGGCTGCAGCTGGACT	998
Qy	281	GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProProGluLys	300
Db	999	GGCACAGTGACGGCGCGTGTACCCAGGAGCCGGGCCCGCCGCCGCCGCGAGAG	1058
Qy	301	GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly	320
Db	1059	GAGCAGCCACTG-----CTGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC	1106
Qy	321	ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer	340
Db	1107	AGGCCCGGATCCCTCTTCCGCCCGGAGAGGCTCAGCGGCTTCCCGGCCACGGCTCG	1166
Qy	341	AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer	360
Db	1167	GCCTGTGATTATCCAGCAGAACTTGGCTTCATCGACGAGTCTTCGGATACGCAGAGC	1226
Qy	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys	380
Db	1227	GAGCGCGCTGCGCGTGCCTCCGCGCGCAGAGGTGCGCGCCGCCCAATCCCCCAGG	1286
Qy	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398
Db	1287	AGCCCCGTGGCGCCCGCGCGCTCCCGCGAGACAAAGCGTGCCTGGTG	1340
RESULT	10		
ADH51638			
ID	ADH51638	standard; cDNA; 1408 BP.	
XX	AC	ADH51638;	
XX	DT	25-MAR-2004 (first entry)	
XX	XX	Human 12303 protein cDNA sequence.	
DE	XX	cytostatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;	
KW	KW	respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;	
KW	KW	immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;	
KW	KW	antianemic; endocrine-Gen; neuroprotective; nootropic; cardiac;	
KW	KW	gene therapy; cellular proliferative; differentiative disorder; brain;	
KW	KW	blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;	
KW	KW	pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;	
KW	KW	immune disorder; inflammatory disorder; cardiovascular disorder;	
KW	KW	endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesis;	
KW	KW	neoplastic; endocrine disorder; neurological; heart; tissue typing;	

chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;  
ss; 12303.  
XX Homo sapiens.  
OS  
XX US2003219806-A1.  
PN  
XX 27-NOV-2003.  
PD  
XX 18-MAR-2003; 2003US-00391399.  
PF  
XX 22-FEB-2000; 2000US-00510706.  
PR 07-APR-2000; 2000US-0195734P.  
PR 31-MAY-2000; 2000US-00583373.  
PR 26-JUN-2000; 2000US-0214176P.  
PR 08-AUG-2000; 2000US-0063466P.  
PR 31-AUG-2000; 2000US-0229036P.  
PR 19-SEP-2000; 2000US-0233537P.  
PR 01-FEB-2001; 2001US-0267076P.  
PR 20-FEB-2001; 2001US-00789481.  
PR 12-MAR-2001; 2001US-0275172P.  
PR 06-APR-2001; 2001US-00828035.  
PR 26-JUN-2001; 2001US-00891762.  
PR 25-AUG-2001; 2001US-00942447.  
PR 17-SEP-2001; 2001US-0322983P.  
PR 19-SEP-2001; 2001US-00957683.  
PR 27-SEP-2001; 2001US-0325854P.  
PR 04-DEC-2001; 2001US-0336936P.  
PR 31-JAN-2002; 2002US-00062937.  
PR 08-MAR-2002; 2002US-00094214.  
PR 11-MAR-2002; 2002US-00095139.  
PR 17-SEP-2002; 2002US-00245121.  
PR 26-SEP-2002; 2002US-00255532.  
PR 04-DEC-2002; 2002US-00309804.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Gluckemann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;  
PI  
XX WPI; 2004-010868/01.  
DR P-PSDB; ADH51639.  
XX  
XX New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,  
PT 55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,  
PT useful for diagnosing, preventing or treating e.g. proliferative or brain  
PT disorders.  
XX  
XX Claim 1; SEQ ID NO 18; 276pp; English.  
PS  
XX This invention relates to novel human DNA sequences (designated 18607,  
CC 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,  
CC 52991, 59914, 59921 or 33751) and the proteins encoded by them. The  
CC invention may be useful for the development of compounds with a  
CC cytosolic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen,  
CC respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,  
CC immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic,  
CC antianemic, endocrine-Gen, neuroprotective, nootropic or cardiac  
CC activity. In addition, the sequences may be useful for gene therapy. The  
CC invention may be useful in diagnosing, preventing or treating disorders  
CC characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433,  
CC 38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for  
CC example cellular proliferative and/or differentiative disorder, brain  
CC disorder, blood vessel disorder, platelet disorder, breast disorder,  
CC colon disorder, kidney disorder, lung disorder, ovarian disorder,  
CC prostate disorder, pancreatic disorder, skeletal muscle disorder,  
CC testicular disorder, hormonal disorder, disorder associated with bone  
CC metabolism, immune disorder, inflammatory disorder, cardiovascular  
CC disorder, endothelial cell disorder, liver disorder, viral disease, pain,  
CC metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder,  
CC endocrine disorder, neurological disorder or heart disorder. They may  
CC also be used in screening assays, tissue typing, chromosomal mapping,  
CC predictive medicine or pharmacogenomics. The present sequence is that of

CC the cDNA which encodes the human 12303 protein of the invention.  
XX  
SQ Sequence 1408 BP; 204 A; 500 C; 459 G; 245 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 4, 12e-84 Length: 1408  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 12 Gaps: 2  
  
US-09-655-272-2 (1-398) x ADH51638 (1-1408)  
QY 1 MetArgSerThrLeuLeuAlaLeuValLeuLeuValSerGly 20  
DB 162 ATGCGCAGCACCACGCTCTGCGCCCTGCTGGCGCTGCTGTTTCTTACTTGGTCTGGT 221  
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
DB 222 GCCTGTGTTCGGGGCCCTGGAGCAGCCCCACGAGCAGCAGCCAGAGGAGCTGGG 281  
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
DB 282 GAGGTCCGAGAGAGTTCCTGAGGGCCCATCCGTGTGTGAGCGACACGAGGAGCTGGCCTC 341  
QY 61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
DB 342 CTCATCAAGAGGTGGCTGATGCCCTGGAGGGGTGGGACCCAGAAACCACTCGACC 401  
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
DB 402 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGCAGCGCTCTCTTTCTCAGGGACC 458  
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
DB 459 ATCATCACCACCATCGGCTATGCAATGTGGCCCTGCGCACAGATCCCGGCGCCTCTTC 518  
QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
DB 519 TGCATCTTTATGCGCTGTGTGGGATTCGCTGTGTGGATCTCTACTGCGAGGGGTGGG 578  
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
DB 579 GACCGCTGGGCTCTCTCCCTGCGCCATGCATCGGTGCACATTGAAGCCATCTCTTGAAG 638  
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
DB 639 TGGCAGCTGCCACCGGAGCTAGTAGAGTGTGTGGCGATGCTTTTCTGTGATCGGC 698  
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
DB 699 TGCCTCTCTTTGTCTCTACGCCACCTTCGTGTCTGCTATATGAGGACTGGAGCAAG 758  
QY 201 LeuGluAlaIleThrPheValIleValThrLeuThrThrValGlyPheGlyAspThrVal 220  
DB 759 CTGGAGGCCATCTACTTGTTCATAGTACGCTTACCACCGTGGCTTTGGCGACTATGTG 818  
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValThrPheTrpIle 240  
DB 819 GCCGGCGCGAGACCCAGGAGGAGACTCCCGGCTATCAGCCGCTGTGTGTGTCTGGATC 878  
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
DB 879 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGAACTGGCTGCAGTA 938  
QY 261 ValSerArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaIleSerTrpThr 280  
DB 939 GTGTCCCGGCACCTCGGCGAGATGGGGCGGCTCAGCGCTCAGGCTGCAGCTGAGACT 998  
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
DB 999 GGCACAGTGACAGCGCGCTGACCCAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGAG 1058



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QY 161 TtpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuLeuGly 180
Db 639 TGGACGCTGCCACCGAGCTAGTAAGAGTCTCTCGCGCATGCTTTCTGCTGATCGGC 698
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 699 TGCCTGCTCTTGTCTCTACGCCACCGTTCGTGTTCTGTATATGAGGACTGGAGCAAG 758
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 759 CTGGAGGCATCTACTTTGTATGATGACGCTTACACCGTGGCTTTGGCGACTATG 818
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 819 GCGGCGCGGACCCAGGAGGACTCCCGCGCTATCAGCGCTGTGTGTCTGATC 878
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 879 CTGCTCGGCTGCTTACTTCGCTCAGTGCTCACCACCATCGGAACTGGCTGCGAGTA 938
QY 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 939 GTGTCGCGGCACTCGGCGAGATGGCGGCTCAGGCTCAGGCTGCCAGCTGGACT 998
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGACAGCGCGTGACCCAGGAGCGCGCGCGCGCGCGCGCGGAG 1058
QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValGluProAlaGly 320
Db 1059 GAGCAGCCACTG-----CTGCTTCCACCGCTTCCAGCGCAGCGCGTGGGC 1106
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 1107 AGGCCCGGATCCCTTCGCCCCCGGAGAGGCTCAGCGGCTTCCCGCCACGCGCTCG 1166
QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1167 GCCTTGGATTATCCAGCGAGAACCTGGCTTCATCGAGAGTCTCTCGGATACGAGAGC 1226
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380
Db 1227 GAGCGCGGCTGCGCTGCGCGCGCGCGCGAGAGTCTCGCGCGCCCAATCCCGCAGG 1286
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1287 AAGCCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1340
```

## RESULT 12

AAD58498  
ID AAD58498 standard; DNA; 2772 BP.

AC AAD58498;

XX 04-DEC-2003 (first entry)

XX Human potassium channel, KCNK4 DNA.

XX Human; urological disorder; urinary incontinence; gene therapy; cancer;  
KW kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;  
KW urethra; overflow urinary incontinence; stress urinary incontinence;  
KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;  
KW potassium channel; KCNK4; gene; ds.

XX Homo sapiens.

XX Location/Qualifiers

FF 64..1323

FT /tag= a

FT /product= "Human potassium channel"

FT /note= "The CDS is referred to as SEQ ID NO:45 in the  
specification"

XX XX

PN W02003061573-A2.  
XX 31-JUL-2003.  
XX 16-JAN-2003; 2003WO-US001450.  
XX 18-JAN-2002; 2002US-0349511P.  
PR 28-FEB-2002; 2002US-0360500P.  
PR 15-MAR-2002; 2002US-0365041P.  
PR 19-APR-2002; 2002US-0374063P.  
PR 14-AUG-2002; 2002US-0403468P.  
PR 27-SEP-2002; 2002US-0414262P.  
PR 21-OCT-2002; 2002US-0419986P.  
PR 05-NOV-2002; 2002US-0423809P.  
PR 26-NOV-2002; 2002US-0429797P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Silos-Santiago I, Karicheti V;  
PI P-PSDB; AAE38597.  
DR WPI; 2003-598705/56.  
XX P-PSDB; AAE38597.

PT Identifying a compound for treating urological disorders, for example  
PT urinary incontinence by assaying the ability of the compound to modulate  
PT the nucleic acid expression or polypeptide activity.

XX Disclosure; Page 194-195; Opp; English.

XX The present relates to a method for identifying a compound for treating  
CC urological disorders e.g., urinary incontinence including overactive/  
CC oversensitive bladder, overflow urinary incontinence, stress urinary  
CC incontinence caused by dysfunction of the bladder, urethra or central  
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,  
CC cancer of the prostate or kidney disorders. The method is also useful for  
CC modulating hyperplasia in a cell and treating a subject having a  
CC urological disorder. The invention is also used in gene therapy. The  
CC present sequence is human potassium channel, KCNK4 DNA

XX Sequence 2772 BP; 521 A; 911 C; 868 G; 472 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8-27e-84 Length: 2772  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
D: 10 Gaps: 2

US-09-655-272-2 (1-398) x AAD58498 (1-2772)

QY 1 MetArgSerThrThrLeuLeuAlaLeuAlaLeuValLeuLeuValSerGly 20  
Db 142 ATGCGGACGACGACGCTCTGCGGCTGCTGCTTACTTGTGTCTGT 201  
QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40  
Db 202 GCCTGTGTTCGGGCGCTGGAGCAGCCGAGCAGCAGCAGCAGGAGGAGCTGGG 261  
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
Db 262 GAGGTCCGAGAGAGTCTCTGAGGCGCCATCCGCTGTGTGAGCGACCCAGGAGCTGGCCCTC 321  
QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
Db 322 CTCATCAGAGGAGTGGCTGATGCCCTGGAGGGGGTGGAGCCCAACCACTCGACC 381  
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
Db 382 AGCAACAGCAGCCAC--TCAGCCTGGGACCTGGGCGAGCGCTCTCTTTCTCAGGAGCC 438  
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120



QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuLeuHisThrAspAlaGlyArgLeuPhe 120  
Db 439 ATCATCACCACCATCGGCTATGCAATGGCCCTGCGCACAGATCCCGGGCGCTTC 498  
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db 499 TGCATCTTTATCGCTGGTGGGATTCGCTGTTGGGATCTACTACGAGGGGTGCGG 558  
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db 559 GACCGGCTGGGCTCTCCCTCGGCCATGCGTCATCGGTACATTGAGCCATCTCTTGAAG 618  
QY 161 TrpHisValProGlyIleValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
Db 619 TGCACGTGCCACCGAGCTAGTAAGAGTGTGCGGATGCTTTCTGCTGATCGGC 678  
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
Db 679 TGCCTGCTTGTCTCAGCCGCCACGTTCGTGTTCTGTATATGAGGACTGGAGCAAG 738  
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220  
Db 739 CTGGAGGCCATCTACTTGTTCATAGTACGCTTTACCACCGTGGGCTTTGCGCACTATGTG 798  
QY 221 ProGlyAspGlyThrGlyGlnAenSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
Db 799 GCCGGCGGACCCCGAGAGTCTCCCGGCTATCAGCGCTGTGTGTCTGATC 858  
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
Db 859 CTGCTCGGCTGCTTACTTCTGCTCAGTGTCTCAGTGTCTCACCACCATCGGAATGGCTCGAGTA 918  
QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaSerTrpThr 280  
Db 919 GTGTCCCGCGCATCTCGGCGAGATGGCGGCTTCACGGCTCAGGCTGCCAGCTGGACT 978  
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
Db 979 GGCACAGTGACGGCGCTGACCCAGCGAGCGCGGCGCCCGCCCGCGCGGAGAG 1038  
QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
Db 1039 GAGCAGCCTG-----CTGCTCCACCGGCTGTCCAGCGCAGCGCGTGGG 1086  
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340  
Db 1087 AGGCCCCGATCCCTTCGCCCCCGAGAGGCTCAGCGGCTTCCCGCCCGCAGGCTCG 1146  
QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
Db 1147 GCCCTGATTTATCCAGCGAGAACCTTGCCTTCATCGACGAGTCTCGGATACGAGAGC 1206  
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAnProSerLys 380  
Db 1207 GAGCGCGCTGCCGCTGCCCGCGCGCGAGAGTCCGCGCGCCCAAAATCCCCCGAG 1266  
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
Db 1267 AAGCCCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1320

RESULT 14  
ID ABX91950 standard; cDNA; 3945 BP.  
XX AC ABX91950;  
XX DT 08-MAY-2003 (first entry)  
XX DE Human G protein-coupled receptor-like (GPCR-like) cDNA #20.  
XX KW Human; G protein-coupled receptor; GPCR; gene; ss; ophthalmic disease;  
KW neurological disease; immunological disease; nephritic disease; cancer;

hormonal dysfunction; neoplasm; atherosclerosis; diabetes; chemotherapy;  
anemia; irradiation; erythroid precursor; erythroid cell; ulcer; organ;  
pressure ulcer; vascular insufficiency; surgical wound; traumatic wound;  
pancreas; liver; intestine; kidney; skin; endothelium; skeletal muscle;  
smooth muscle; cardiac muscle; vascular tissue.  
Homo sapiens.  
US2002146692-A1.  
10-OCT-2002.  
21-DEC-2000; 2000US-00747835.  
21-JAN-2000; 2000US-00488725.  
25-APR-2000; 2000US-00552317.  
20-JUN-2000; 2000US-00598042.  
19-JUL-2000; 2000US-00620312.  
31-AUG-2000; 2000US-00653450.  
04-DEC-2000; 2000US-00729739.  
(YAMA/) YAMAZAKI V.  
(TANG/) TANG Y T.  
(LIUC/) LIU C.  
(ZHOU/) ZHOU P.  
(WANG/) WANG D.  
(ZHAN/) ZHANG J.  
(REN/) REN F.  
(ASUN/) ASUNDI V.  
(DRWA/) DRWANAC R T.  
Yamazaki V, Tang YT, Liu C, Zhou P, Wang D, Zhang J, Ren F;  
Asundi V, Drmanac RT;  
WPI; 2003-174164/17.  
Isolated polynucleotide for treating, e.g. ophthalmic diseases, comprises  
specified nucleotide sequences, or their translated protein coding  
portion, mature protein coding portion, extracellular portion, or active  
domain.  
Claim 1; Page 100-102; 158pp; English.  
The invention relates to human G protein-coupled receptor-like (GPCR-  
like) proteins and the polynucleotides encoding them. The isolated  
sequences are used for the treatment of diseases of ophthalmic,  
neurological, immunological, or nephritic systems. They may also be used  
to treat hormonal dysfunction, cancer and other neoplasia,  
atherosclerosis, diabetes, in treating various anaemias or for use in  
conjunction with irradiation/chemotherapy to stimulate the production of  
erythroid precursors and/or erythroid cells. The sequences may be used to  
promote better or faster closure of non-healing wounds, including  
pressure ulcers, ulcers associated with vascular insufficiency and  
surgical and traumatic wounds and in generation or regeneration of other  
tissues, e.g. organs (e.g. pancreas, liver, intestine, kidney, skin,  
endothelium), muscle (smooth, skeletal, or cardiac) and vascular tissue  
or for promoting the growth of cells comprising such tissues. Sequences  
or ABX91935-ABX91958 represent human GPCR-like polynucleotides of the  
invention  
Sequence 3945 BP; 606 A; 1344 C; 1238 G; 757 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,97e-83 Length: 3945  
Score: 1688.50 Matches: 327  
Percent Similarity: 88.41% Conservative: 24  
Best Local Similarity: 82.37% Mismatches: 41  
Query Match: 81.22% Indels: 5  
DB: Gaps: 2  
US-09-655-272-2 (1-398) x ABX91950 (1-3945)  
QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuTyrLeuValSerGly 20







Length:	1182
Matches:	328
Conservative:	24
Mismatches:	41
Indels:	5
Gaps:	2

```

381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
1126 AAGCCCTCGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1179

RESULT 2
US-09-432-470-3
Sequence 3, Application US/09432470
Patent No. 6426197
GENERAL INFORMATION:
APPLICANT: David Malcolm Duckworth
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCES: GP-30190
CURRENT APPLICATION NUMBER: US/09/432,470
CURRENT FILING DATE: 1999-11-03
EARLIER APPLICATION NUMBER: UK 9923668.9
EARLIER FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: UK 9824048.4
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1218
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-432-470-3

Alignment Scores:
Pred. No.: 2,53e-124 Length: 1218
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 4 Gaps: 2

US-09-655-272-2 (1-398) x US-09-432-470-3 (1-1218)

QY 1 MetArgSerThrThrLeuAlaLeuAlaLeuValLeuLeuLeuValSerGly 20
DB 37 ATGCGGAGCACCACCTCTCTGGCCCTGCTGGCGTGGTCTTCTTCTTCTTCTG 96
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGlnGlnAlaGlnLysMetAsp 40
DB 97 GCCTTGGTGTTCGGCGCCCTGGAGCAGCCCCACGAGCAGGCGCCAGAGAGCTGG 156
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 157 GAGGTCCGAGAGAGAGTTCCTGAGGCCCATCGTGTGTGAGCGACCCAGAGCTGG 216
QY 61 PheIleLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
DB 217 CTATCAAGGAGGTGGCTGATGCTTGGGAGGGGTGGGACCCAGAACCCAGCTG 276
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
DB 277 AGCAACAGCAGCCAC---TCAGCCTGGACCTTGGGAGGCGCTTCTTTCTCAGG 333
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
DB 334 ATATCAACACCATCGGTATGCAATGTGGCTGCTGGCAGATGCCCGGCGCTTTC 393
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuAlaGlyValGly 140
DB 394 TGCATCTTTATGCGTGGTGGGATTCGCGCTGTGTGGGATCTCTACTGGCAGGG 453
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 454 GACCGCTGGGCTCTCTCCCTGCCCATGGCATCGGTGCATTCATTGAGCCATCTT 513
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuLeGly 180
DB 514 TGGCAGCTGCCACCGGAGCTAGTAAGAGTGTCTGCGCGAGTGTCTTTCTGCTG 573
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Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 574 TGCTGTCTTGTTCCTCAGCCACCGTTCGTGTCTATATGAGGAGCTGGAGCAAG 633
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 634 CTGGAGGCCATCTACTTGTTCATAGTAGCGCTTACCAACCGTGGCTTTGGGCACTATGTG 693
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 694 GCCGGCGCGGACCCAGCAGGACTCCCGCGCTATCAGCGCTGTGTGTCTGGATC 753
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 754 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTACCAACCATCGGAACTGGCTCGAGTA 813
Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 814 GTGTCCCGCGCACTCGGCGAGAGATGGCGGCTCTACGGCTCAGGCTGCAGCTGGACT 873
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 874 GGCACAGTGACAGCGCGTGCACCGAGCGCGGCGCGCGCGCGCGCGCGCGCGAGAG 933
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 934 GAGCAGCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 981
Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 982 AGGCCCGCATCCCTTCGCCCCCGAGAGGCTCGCGGCTTCCCCCGCCACGCGCTCG 1041
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1042 GCCCTGATTATCCAGCGAGAACCTGCGCTTCATCGACGAGTCTCGGATACGAGAGC 1101
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 1102 GAGCGCGGCTGCCGCTGCCCGCGCGCGCGAGAGGTGCGCGCGCCCAATCCCGCCAGG 1161
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1162 AGCCCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1215
```

## RESULT 3

```
US-09-620-312D-195
; Sequence 195, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
```

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; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 195
; LENGTH: 3996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3996)
US-09-620-312D-195

Alignment Scores: 2.83e-123 Length: 3996
Pred. No.: 1688.50 Matches: 327
Score: 88.41% Conservative: 24
Percent Similarity: 82.37% Mismatches: 41
Best Local Similarity: 81.22% Indels: 5
Query Match: 4 Gaps: 2
DB:

US-09-655-272-2 (1-398) x US-09-620-312D-195 (1-3996)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20
Db 1669 ATCGCGAGCACCACGCTCTCGGCCCTGCTGGCGCTGCTTGTCTTGTGTCTGGT 1728
Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40
Db 1729 GCCTCTGTGTTCGGGCGCTCGAGAGAGCCACAGCAGCAGCAGCAGGAGCTGGGG 1788
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 1789 GAGGTCCGAGAGAGTTCCTGAGGGCCCATCCGTGTGTGAGCGACAGGAGCTGGGCTC 1848
Qy 61 PheIleValLeuLeuValGluAlaLeuGlyGlyAlaAsnProGlnThrSerTrpThr 80
Db 1849 CTCATCAAGAGAGGTGGCTGATGCCCTGGGAGGGGGTGGCGACACCACTCGACC 1908
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 1909 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1965
Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 1966 ATCATCACCACCATCGCTATGGCAATGCGCCCTGCGCACAGATGCGCGGCGCTCTTC 2025
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 2026 TGCATCTTTATGCGCTGGTGGGGATTCGCTGTTTGGGATCTCTACTGGCAGGGGTGGG 2085
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 2086 GACCGCGTGGCTCTCTCCCTGCGCCATGGATCGCATCGATGAGCCATCTTCTTGAAG 2145
Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
Db 2146 TGGCAGTGGCCACCGGAGCTAGTAAAGAGTGTCTGCGCGATGCTTTTCTGCTGATCGGC 2205
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 2206 TGCCTGCTCTTGTCTCAGCGCCACGTTCTGCTGTATATGAGGAGCTCGAGCAAG 2265
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 2266 CTGGAGGCCATCTACTTGTTCATAGTAGCGCTTACCAACCGTGGGCTTGGGCACTATGTG 2325
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 2326 GCCGGCGCGGAGCCCGCAGGAGGACTCCCGCGCTATCAGCGCTGTGTGTGTCTGGATC 2385
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
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Db      2386 CTGCTCGGCTGGCTTACTTGGCTCAGTGTCTCAGCACCACATCGGAATCGGTGGAGTA 2445
Qy      261 ValSerArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db      2446 GTGTCCGCGGACCTCGGCGAGAGTGGCGGCTCAGGCTCAGGCTGCCAGCTGGACT 2505
Qy      281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db      2506 GGCACAGTGACAGCGGCGGTGACCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGGAG 2565
Qy      301 GluGlnProLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320
Db      2566 GAGCAGCCACTG-----CTGCTTCCACCGCCCTGTCCAGCGCAGCGCGTGGGC 2613
Qy      321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db      2614 AGGCCCGATCCCTTCGCCCCCGGAGAGGCTCAGCGCTTCCCGCGCCAGCGCTCG 2673
Qy      341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db      2674 GCCCTGATATTATCCAGCGAGAACCTGGCCCTTCATGACGAGTCTCCGATACGACAGC 2733
Qy      361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db      2734 GAGCGCGCTGCCGCTGCCCGCGCGCGCGCGAGAGTCCGCGCGCCCAATCCCGCCAGG 2793
Qy      381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValPro 397
Db      2794 AAGCCCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2844

```

RESULT 4

US-09-799-451-432  
; Sequence 432, Application US/09799451  
; Patent No. 6783969

GENERAL INFORMATION:

```

; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 432
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (473) ..(2086)

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US-09-799-451-432

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Alignment Scores:
Pred. No.: 1,83e-54 Length: 2730
Score: 812.00 Matches: 179
Percent Similarity: 56.21% Conservative: 61

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Best Local Similarity: 41.92% Mismatches: 132
Query Match: 39.06% Indels: 55
DB: 4 Gaps: 7
US-09-655-272-2 (1-398) x US-09-799-451-432 (1-2730)
Qy      1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20
Db      671 ATGAAGTAGGAGACGGTGGTGGTCATCTTTGGTGGTGGTGGTGGTGGTGGTGGTGG 730
Qy      21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
Db      731 GGTCTTCTTCCTCGGCGCATTTGGAGCAGCCCTTTGAGAGCAGCCAGAGATACCATCGCC 790
Qy      41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db      791 TTGAGAGAGCGGGAATTCCTCGGGATCATGTCTGTGTGAGAGCCCGCAGGAGCTGGAG 850
Qy      61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80
Db      851 TTGATCCAGCATGCTCTTGATGTGACAATCGGGAGTCTAGTCCA-----ATAGGA 901
Qy      81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db      902 AACTCTTCCAAACACAGCAGCAGCCTGGGACCTCGCAGTGCCTTTTCTTGTGGAACT 961
Qy      101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db      962 GTCAATTACGACCATAGGTATGGGAATATTGCTCCGAGCAGCTGAAGAGGCAAAATCTTT 1021
Qy      121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db      1022 TGTATTTTATATGTCATCTTTGGAAATTCACCTCTTTGGTTCTTATTGGCTGGAAATGGA 1081
Qy      141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db      1082 GACCAACTTGGACCATCTTTGGGAAAGCATTTGCAAGAGTGGAGAGGTCTTTTCGAAA 1141
Qy      161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuLeuPheLeuIleGly 180
Db      1142 AAGCAAGTGAAGTCAGCAGCAAGATCCGGGTCTATCAACCATCTCTGTTCTATCTTGGCCGC 1201
Qy      181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db      1202 TGCATTGTGTTTGTGACGATCCCTGCTGCTCATCTTTAAGTATACATCGAGGCTGGACGCC 1261
Qy      201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db      1262 TTGGAGTCCATTTACTTTTGTGTGTGTCTCTGACCCCGTGGGCTTTGGTGAITTTGTG 1321
Qy      221 ProGlyAspGlyThrGlyGlnAsn---SerProAlaTyrGlnProLeuValTrpPheTrp 239
Db      1322 GCAGGGGAAACGCTGGCATCAATATTCGGGAGTGGTATAGCCCTAGTGTGGTTTGG 1381
Qy      240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArg 259
Db      1382 ATCTTTTGGCTTGCCTTACTTTGAGTGTCTCTCAGTATCATCGGAGATGGGTACGG 1441
Qy      260 AlaValSerArgArgThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrp 279
Db      1442 GTTCTGTCCAAAAGACAAAGAGAGGTGGGTGAATCAAGGCCCATCGGCAGAGTGG 1501
Qy      280 ThrGlyThrValThrAlaArgVal----- 287
Db      1502 AAGGCCAATGTACCGCTGAGTTCGCGGAGACACGCGGAAGGCTCAGCGTGGAGATCCAC 1561
Qy      288 -----ThrGlnArgThrGly-ProSerAlaPro----- 296
Db      1562 GATAAGCTGCAGCGCGCGCCACCATCCCGCAGCATGGAGCGCGCGGTGGCCCTGGAC 1621
Qy      297 -----ProProGluLysGluGlnProLeuLeuProse 307
Db      1622 CAGCGGGCCCACTCACTGGACATGCTGTCCCGGAGAGCGGCTCTGTCTTTGTGCTGCTG 1681

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QY 307 rSerLeuProAlaProProAlaValValGluProAlaGlyArgProGlySerProAlaPr 327
Db 1682 GACA-----CCGCCCGCTTCAAGCGCTCATCCAGG----- 1712

QY 327 oAlaGluLysValGluThrProSerProThrAlaSerAlaLeuAspTyrProSerGI 347
Db 1713 -----AGAGCATCAACAACCGGCCCAACACCTCGCCCTGAAGGGCGGAGCAGCTG 1765

QY 347 uAsnLeuAlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCysAlaLeuPr 367
Db 1766 AACAGCATCGGCGAGGTGGTCCGAGGACAAACATCATCAACAGTTCGGGTCCACCTCC 1825

QY 367 oArgAlaProArgGlyArgArg-----ProAsnProSerLysly 381
Db 1826 AGACTCACCAAGAGGAAAAAACAAGGACCTCAAAAAGACCTTGCCCGAGGAGCGTTTCAGAA 1885

QY 381 sProSerArgProArgGly 387
Db 1886 ATCTACAAGACCTTCGCGA 1904

RESULT 5
US-09-236-080-5
; Sequence 5, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25,
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-236-080-5

Alignment Scores:
Pred. No.: 1.88e-52 Length: 1994
Score: 784.00 Matches: 161
Percent Similarity: 62.04% Conservative: 58
Best Local Similarity: 45.61% Mismatches: 111
Query Match: 37.71% Indels: 23
DB: 3 Gaps: 3

US-09-655-272-2 (1-398) x US-09-236-080-5 (1-1994)

QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGly 20
Db 607 ATGAATGGAAGACAGTCTCCAGCATTTCTCGTGTGCTCTCTACCTGATCATCGGA 666

QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
Db 667 GCCCGCGTGTTCAGGCATTTGAGCAGCTCCAGCAGATTTCCCGAGAGACCACTTTGTG 726

QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 727 ATCCAGAAAGCAGACCTTCATAGCCCGCAGCATGCTGCGTCAACTCCACCGAGCTGGACGAA 786

QY 61 PheIleLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 787 CTATCCAGCAATAGTGGCAGCAATAAACGCGGGATTATCCCT-----TTAGGA 837

QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 838 AACAGCTCCAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTCTTTGCTGTACT 897

QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 898 GTTATCAACACCATAGGATTTGGAAACATCTCCCAAGAACTGAAAGGTGGAATAATTC 957

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QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 958 TGCAATCATCTATGCTTGTCTGGAAATTCCTCTTTGGCTTTCTACTGGCTGGGTGGT 1017

QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 1018 GATCAGCTAGGAACATATATTGGAAAGGAATTCGCAAGATGGAGACACATTTATTAG 1077

QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuLeu 180
Db 1078 TGGATGTTAGTCAGAGGAAGATTGATATCATCTCCACCATCATCTTCCTGTTTGGC 1137

QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 1138 TGTGTCTCTTGTGTGCTCTCCCTGCGGTCAATATTCAAGCACATAGAAGCTGGAGCGCC 1197

QY 201 LeuGluAlaIleTyrPheValIleValLeuThrThrValGlyPheGlyAspTyrVal 220
Db 1198 CTGGAGCGCTATCTATTTGTGTGTTACTCTGACGACCATTTGGATTTGGAGACTACGTG 1257

QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 1258 GCAGGTGGATCAGACATTCGACTTCTACAGCCTGTGCTGTGTTCTGATC 1317

QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 1318 CTCGTTGGGCTGCGCTTACTTTCAGCTGTTCTGAGCATGATTGGGACTGGCTACGGTG 1377

QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 1378 ATCTCTAAGAGACGAAAGAGGTGGGAGAGTTCCAGAGCGCATGCCCTGATGGACA 1437

QY 281 GlyThrValThrAlaArgValThrGlnArg-----Th 291
Db 1438 GCCAATGTCACGCGCAGTTCAGGAAACGAGGAGCGGCTGAGCGTGAGATCTACGAC 1497

QY 291 rGlyProSerAlaProProProGluLysGluGlnProLeuLeuProSerSerLeuProA 311
Db 1498 AAGTTCAGCGTGGCCACATCCGTAAGCGGAAGCTCTCCGACAGAGCTGGCGGCAACCCAC 1557

QY 311 laPro-----ProAlaValGluProAlaGlyArgProG 323
Db 1558 AACACGAACTGACTCCGTTGATGAGGACCTCTGTGTAACCCCTGACCGACGAGG 1617

QY 323 lysSerProAla-ProAlaGluLysValGluThr 333
Db 1618 GAAGTCTGCTCCCTCCCTTGTGTAAGGCTGAGAGC 1650

RESULT 6
US-09-236-080-1
; Sequence 1, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-236-080-1

Alignment Scores:
Pred. No.: 2.86e-52 Length: 1246
Score: 778.00 Matches: 149
Percent Similarity: 67.53% Conservative: 59
Best Local Similarity: 48.38% Mismatches: 87

```

```

GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1285)
; US-09-336-643A-82

Alignment Scores:
Pred. No.: 1,14e-51 Length: 3300
Score: 778.00 Matches: 149
Percent Similarity: 67.53% Conservative: 59
Best Local Similarity: 48.38% Mismatches: 87
Query Match: 37.42% Indels: 13
DB: 3 Gaps: 3

US-09-655-272-2 (1-398) x US-09-336-643A-82 (1-3300)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuValSerGly 20
DB 173 ATGAAATGGAAGACGGTCTCCACGATATTCTCTGGTGGTGGTCTCTATCTGATCGGA 232
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnLysMetAsp 40
DB 233 GCACCGGTCTTCAAGCATTTGGAGCAGCTCATGAGATTTCCAGAGGACCCATTGTG 292
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 293 ATCCAGAGCAACATTCATATCCCAACATCTCTGTGCAATTCACGAGCTGGATGAA 352
QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80
DB 353 CTATTTCAGCAATAGTGGCAGCAATAATGCGAGGATTATACCG-----TTAGGA 403
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr 100
DB 404 AACACCTCCAATCAATCAGTCAGTGGATTTGGGAAGTTCCTCTCTTCTGCTGCACT 463
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
DB 464 GTTATTACCAACCATAGATTTGGAAACATCTCCACCGCAGCAGAGCGGCAAAATATTC 523
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuValGly 140
DB 524 TGTATCATCTATGCCTTACTTGGGAATTCCTCTTTGGTTTCTCTGCTGGAGTTGA 583
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 584 GATCAGCTAGGCACCATATTTGGAAAGGAATTTCCAAAGTGGAGATGATTATTAAAG 643
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
DB 644 TGGAAATGTAGTCAGACCAAGATTGCGCATCTCTCAACATCATATTTATTATTTGGC 703

; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1285)
; US-09-336-643A-82

Alignment Scores:
Pred. No.: 1,14e-51 Length: 3300
Score: 778.00 Matches: 149
Percent Similarity: 67.53% Conservative: 59
Best Local Similarity: 48.38% Mismatches: 87
Query Match: 37.42% Indels: 13
DB: 3 Gaps: 3

US-09-655-272-2 (1-398) x US-09-336-643A-82 (1-3300)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuValSerGly 20
DB 173 ATGAAATGGAAGACGGTCTCCACGATATTCTCTGGTGGTGGTCTCTATCTGATCGGA 232
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnLysMetAsp 40
DB 233 GCACCGGTCTTCAAGCATTTGGAGCAGCTCATGAGATTTCCAGAGGACCCATTGTG 292
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 293 ATCCAGAGCAACATTCATATCCCAACATCTCTGTGCAATTCACGAGCTGGATGAA 352
QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80
DB 353 CTATTTCAGCAATAGTGGCAGCAATAATGCGAGGATTATACCG-----TTAGGA 403
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr 100
DB 404 AACACCTCCAATCAATCAGTCAGTGGATTTGGGAAGTTCCTCTCTTCTGCTGCACT 463
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
DB 464 GTTATTACCAACCATAGATTTGGAAACATCTCCACCGCAGCAGAGCGGCAAAATATTC 523
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuValGly 140
DB 524 TGTATCATCTATGCCTTACTTGGGAATTCCTCTTTGGTTTCTCTGCTGGAGTTGA 583
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 584 GATCAGCTAGGCACCATATTTGGAAAGGAATTTCCAAAGTGGAGATGATTATTAAAG 643
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
DB 644 TGGAAATGTAGTCAGACCAAGATTGCGCATCTCTCAACATCATATTTATTATTTGGC 703

; RESULT 7
; US-09-336-643A-82
; Sequence 82, Application US/09336643A
; Patent No. 6399761

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Thu Feb 3 07:31:01 2005

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QY 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355
Db 1218 CGCCAGGAGTACCCACCTCATCTTCAGGAGCGCCAGCATCACCTTCGTGAACAGGA 1277
QY 355 rSerAsp-ThrGlnSerGluArgCysAlaLeuProArgAlaProArg----- 371
Db 1278 GGCTGGCTCTCAGCAGAGAGA-----CCTCAAGTCTCTCGCTAGAGACAA 1325
QY 372 -----GlyArgAspGluArgProAsnProSerLysLysProSerArgPro 385
Db 1326 CTTGGCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1375

RESULT 9
US-09-431-367B-3
; Sequence 3, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431.367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1497)
US-09-431-367B-3

Alignment Scores:
Pred. No.: 2,258-25 Length: 1497
Score: 438.00 Matches: 130
Percent Similarity: 43.51% Conservative: 78
Best Local Similarity: 27.20% Mismatches: 144
Query Match: 21.07% Indels: 127
DB: 4 Gaps: 16

US-09-655-272-2 (1-398) x US-09-431-367B-3 (1-1497)
QY 9 LeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPheGlnAlaLeuGlu 28
Db 22 CTCACCTCGGCATCATCTTCTACCTGGCCATCGGGCGCGGATCTTCGAAGTGTGGAG 81
QY 29 GlnProHisGluGlnGlnAlaGlnLysLysMetAspHisGlyArgAspGlnPheLeuArg 48
Db 82 GAGCCACACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 141
QY 49 AspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeuValGluAla 68
Db 142 GAGTTCCTGGCTGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 201
QY 69 LeuGlyGlyGlyAlaAsnProGluThrSerTyrThrAsnSerSerAsnHisSerAla 88
Db 202 GCAGGACAGGGT-----GTGGCCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246
QY 89 TrpAsnLeuGlySerAlaPhePheSerGlyThrIleIleThrThrIleGlyTyrGly 108
Db 247 TGAACCTGGCCCAATGCATGATTTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 306
QY 109 AsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheThrAlaLeuValGly 128
Db 307 AATGTGGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
QY 129 IleProLeu-----PheGlyMetLeuLeuAlaGlyValGlyAsp 141
Db 367 GTGCCGCTCTGCTGAGCGTGATGAGTGGCCCTCGGCAAGTCTTCGGGGAGCGTGCCAA 426

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QY 142 ArgLeuGlySerSerLeu---ArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 427 AGACTAGGAGGAGTCTCTTACCAAGAGAGGAGTGTGAGTCTCGCGAAGGCG----- 474
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 475 -----CAGATCAGCTGCACAGTCACTCTTCATCTGTCGTGGTGGGC 510
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTyrSerLys 200
Db 511 GTCCTAGTCCACCTGGTGATCCACCTTCGTATTCATGGTGACTGAGGGGTGGAATC 570
QY 201 LeuGluAlaIleTyrPheValIleValThrThrThrValGlyPheGlyAspTyrVal 220
Db 571 ATCAGGGGCTCTACTACTCTTCATCACCATCTCCACCATCGCTTCGGTGACTTTGTG 630
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAla---TyrGlnProLeuValTyrPheTyr 239
Db 631 GCCGGTGTGAACCCAGCGCCCACTACCGCCCTGTACCGCTACTTCGTGGAGCTCTGG 690
QY 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTyrLeu--- 258
Db 691 ATCTACTTGGGGCTGGCTGG-----CTGTCCCTTTTGTCAACTGGAAGGTG 738
QY 259 -----ArgAlaValSerArgThrArgAla----- 267
Db 739 AGCATGTTTGTGAAGTCCACAAAGCCATTAAAGAGCGCGCGCGCCAGCGAGGAGTCC 798
QY 268 ---GluMetGlyGlyLeuThrAlaGlnAlaAlaSerTyrThrGlyThrValThrAla--- 285
Db 799 TTTGAGAGCTCCACACTCCGGAGGCCCTGCAGGTGAAGGGGAGCAGACGCTCCAAG 858
QY 285 ----- 285
Db 859 GACGTCAACATCTTCAGCTTTCTTCCAAAGAGAGAGACCTTACAAGCCTCATCAAG 918
QY 286 -----ArgValThrGlnArgThr-----GlyProSer 294
Db 919 CAGATCGGGAAGAGCCATGAAGACAAAGCGGGGTGGGAGACGGGCCCGGCCAGGG 978
QY 295 AlaProProGluLysGlnGlnProLeuLeuProSerSerLeuProAlaProAla 314
Db 979 CTGGGGCTCAAGCGGTGGCTCCACGACCTGCCCTTCCCTGCTTCCCTGTGTAGT 1037
QY 315 ValValGluProAlaGly-----Arg 321
Db 1038 CTACTCCAAAGAACCGGGTGCACCTTGAAGAGGTGTCAAGACACTGAGGAGCAAGG 1097
QY 322 ProGly-SerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer-- 340
Db 1098 CCACGTATCAAGTCCCGAGATGAGGAGCTGTGGCAGCGGCCCTTGAAGACAGCTCCC 1157
QY 340 ----- 340
Db 1158 TGCCCCCGAGGTGTTTCATGAACAGCTGGACCGCATCAGCGAGGAATGCGACCATGGA 1217
QY 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355
Db 1218 CGCCAGGAGTACCCACCTCATCTTCAGGAGCGCCAGCATCACCTTCGTGAACAGGA 1277
QY 355 rSerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg----- 371
Db 1278 GGCTGGCTCTCAGAGGAGGAG-----CCTCAAGTCTCTCGCTAGAGACAA 1325
QY 372 -----GlyArgArgProAsnProSerLysLysProSerArgPro 385
Db 1326 CTTGGCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1375

RESULT 10
US-09-561-763-1
; Sequence 1, Application US/09561763
; Patent No. 6664373

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; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(1506)
; US-09-561-763-1

Alignment Scores:
Pred. No.: 7,39e-25 Length: 3452
Score: 438.00 Matches: 130
Percent Similarity: 43.51% Conservative: 78
Best Local Similarity: 27.20% Mismatches: 147
Query Match: 21.07% Indels: 124
DB: 4 Gaps: 16

US-09-655-272-2 (1-398) x US-09-561-763-1 (1-3452)

QY 9 LeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPheGlnAlaLeuGlu 28
DB 31 CTCACCTCGGCCATCATCTTCTACCTGGCCATCGGGCGCGCATCTTCGAAGTCTGGAG 90
QY 29 GlnProHisGluGlnGlnAlaGlnLysMetAspHisGlyArgAspGlnPheLeuArg 48
DB 91 GAGCCACACTGGAAGGAGGCAAGAAACTACTACACACAGAGGCTGCTCAAG 150
QY 49 AspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeuValGluAla 68
DB 151 GAGTTCCTCGGCTGGGTGAGAGGGCTGACAGATCTCAGAGTGGTATCTGATGCT 210
QY 69 LeuGlyGlyAlaAsnProGluThrSerTrpThrAsnSerSerAsnHisSerSerAla 88
DB 211 GCAGGACAGGGT-----GTGGCCATCACAGGGAACAGACCTTCAACAAC--- 255
QY 89 TrpAsnLeuGlySerAlaPhePheSerGlyThrIleIleThrThrIleGlyTyrGly 108
DB 256 TGGAACTGGGCCCAATGCAATGATTTTTCAGCGACCGCTCATACCACTGGATATGGC 315
QY 109 AsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyrAlaLeuValGly 128
DB 316 AATGTGGCTCCCAAGACCCCGCGGTGGCTCTCTCTGTGTCTCTATGCTCTCTTCGGG 375
QY 129 IleProLeu-----PheGlyMetLeuLeuAlaGlyValGlyAsp 141
DB 376 GTGCGGCTCTCGCTGACGTGATCAGTCCGCTGGCAAGTTCTTCGGGGGACGTGCCAAG 435
QY 142 ArgLeuGlySerSerLeu---ArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 436 AGACTAGGCGGAGTTCCTTACCAAGAGAGGTGTAGTCTGCGGAAGGCG----- 483
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
DB 484 -----CAGATCAGCTGCACAGTCACTTCATCGTGGTGGGG 519
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
DB 520 GTCTAGTCCACCTGGTGATCCCACTTCTGATTCATGCTGAGGTGGAACATAC 579
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
DB 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220

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DB 580 ATCGAGGGCTCTACTACTCTCTTTCATCACCATCTCCACCATCGGCTTCGGTGACTTTGTG 639
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrp 239
DB 640 GCGGGTGTGAACCCCGACGCCCACTACCAAGCCCTGTACCGCTACTTCGTGGAGCTCTGG 699
QY 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeu--- 258
DB 700 ATCTACTTGGGGCTGGCTGG-----CTGTCCCTTTTGTCAACTGGAAGGTG 747
QY 259 -----ArgAlaValSerArgArgThrArgAla----- 267
DB 748 AGCATGTTTGTGAAGTCCACAAGCCATTAGAAGCGCGCGCGCGAGGAGGTCC 807
QY 268 ---GluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThrGlyThrValThrAla--- 285
DB 808 TTTGAGAGCTCCCACTCCCGGAAGGCCCTGCAGGTGAAGGGGAGCACAGCTCCAAG 867
QY 285 ----- 285
DB 868 GACGTCAACATCTTCAGCTTTCTTCCAAGAAGAGAGACCTTACAACGACCTCATCAAG 927
QY 286 -----ArgValThrGlnArgThr-----GlyProSer 294
DB 928 CAGATCGGAAGAGGCCATGAAGACACAGCGGGGTGGGAGACGGGCCCGGCCAGGG 987
QY 295 AlaProProGluLysGluGlnProLeuLeuProSerSerLeuProAlaProAla 314
DB 988 CTGGGCGCTCAAGGCGGTGGCTCCCGACGACCTGCCCTTCCCTGCT-GCCCTGTGTAGT 1046
QY 315 ValValGluProAlaGly-----Arg 321
DB 1047 CTACTCCAAGAACCGGTGCCACCTTGAAGAGGTGTACACAGACTGAGGAGCAAGG 1106
QY 322 ProGly-SerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer-- 340
DB 1107 CCACGTATCAAGTCCCCAGATGAGGAGGTGTGGCAGCGGCCCTTGAAGACAGCTCCCC 1166
QY 340 ----- 340
DB 1167 TGCCCCGAGGTGTTTCATGAACAGCTGGACCGCATCAGCGAGGAATCGAGCCATGGGA 1226
QY 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355
DB 1227 CGCCAGGACTACCAACCCACTCATCTTCCAGGACGCCGACATCACCTTCGTGAACACGA 1286
QY 355 rSerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg----- 371
DB 1287 GGCTGGCTCTCAGACGAGAGA-----CCTCAAGTCTCTCGTAGAGNCAA 1334
QY 372 -----GlyArgArgArgProAsnProSerLysLysProSerArgPro 385
DB 1335 CTGGCAGGGGAGGAGAGCCCCCAGCAGCGGGGTGAAGCAAGCGGCCCC 1384
RESULT 11
US-09-431-367B-1
; Sequence 1, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (10) .. (1506)
US-09-431-367B-1

Alignment Scores:
Pred. No.: 7,39e-25 Length: 3452
Score: 438.00 Matches: 130
Percent Similarity: 43.51% Conservatives: 78
Best Local Similarity: 27.20% Mismatches: 144
Query Match: 21.07% Indels: 127
DB: 4 Gaps: 16

US-09-655-272-2 (1-398) x US-09-431-367B-1 (1-3452)
Qy 9 LeuLeuAlaLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPheGlnAlaLeuGlu 28
Db 31 CTACCTCGGCCATCATCTTCTACCTGGCCATCGGGCGGCGATCTTCGAAGTGTGGAG 90
Qy 29 GlnProHisGluGlnGlnAlaGlnLysLysMetAspHisGlyArgAspGlnPheLeuArg 48
Db 91 GAGCCACACTGGAAGGAGGCGCAAGAAACTACTACACAGAGAGCTGCATCTGTCTCAAG 150
Qy 49 AspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeuLeuValGluAla 68
Db 151 GAGTTCGGTCCCTGGGTGAGGCGCTGGACAGATCCTAGAGTGTGTATCTGATGCT 210
Qy 69 LeuGlyGlyGlyAlaAsnProGluThrSerTrpThrAsnSerSerSerAsnHisSerAla 88
Db 211 GCAGACAGAGGT-----GTGGCCATCACAGGGAACAGACCTTCAACAAC--- 255
Qy 89 TrpAsnLeuGlySerAlaPhePheSerGlyThrIleIleThrIleGlyTyrGly 108
Db 256 TGGAACTGGCCCAATGCATGATTTTTCAGCGACCTGATACCACTTGGATGGC 315
Qy 109 AsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyrAlaLeuValGly 128
Db 316 AATGTGGTCCCAAGACCCCGCGTCTCTCTGTGTCTTCTATGTCTCTCTCGGG 375
Qy 129 IleProLeu-----PheGlyMetLeuLeuAlaGlyValGlyAsp 141
Db 376 GTGCGCTCTGCTGACGTGGATCAGTCCCTGGCGCAAGTTCTTCGGGGACGTGCCAAG 435
Qy 142 ArgLeuGlySerSerLeu---ArgArgGlyIleGlyHisIleGlyAlaIlePheLeuLys 160
Db 436 AGACTAGGCGAGTCTCTTACCAAGAGAGGTGTGAGTCTGCGGAAGCG----- 483
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 484 -----CAGATCACTGTCACAGTCATCTTCATCGTGTGGGGC 519
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 520 GTCTAGTACCTGGTATCCACCTTCGTATTCATGCTGACTGAGGGGTGGAAGTAC 579
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 580 ATCAGGGGCTCTACTACTCTTCATCACCATCTCCACATCGGCTTCGGTGAAGTGTG 639
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrp 239
Db 640 GCGGTGTGAACCCCGACGCCCACTACACGCCCTGTACCGCTACTTCGTGAGCTCTGG 699
Qy 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeu--- 258
Db 700 ATCTACTGGGCTGGCTGGCTGG-----CTGTCCCTTTTGTCACTGGAAGGTG 747
Qy 259 -----ArgAlaValSerArgArgThrArgAla----- 267
Db 748 AGCATGTTGTGGAAGTCCACCAAGCCATTAAAGAGCGCGCGCGACGGAAGAGTCC 807
Qy 268 ---GluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThrGlyThrValThrAla--- 285
Db 808 TTGAGAGCTCCCACTCCCGAAGGCCCTGCAGTGAAGGGGACACACGCTCCCAAG 867
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Qy 285 ----- 285
Db 868 GACGTCAACATCTTCAGCTTTCTTTTCAAGAAGAGAGACCTTACAACGACCTCATCAAG 927
Qy 286 -----ArgValThrGlnArgThr-----GlyProSer 294
Db 928 CAGATCGGGAAGAAGGCCATCAAGACAAAGCGGGGTGGGAGACGGGCCCGGCCCGGAGG 987
Qy 295 AlaProProGluLysGluGlnProLeuLeuProSerSerLeuProAlaProAla 314
Db 988 CTGGGGCTCAAGCGGTGGGCTCCAGCACTGCCCTTCCCTTGGT-GCCCTGTGTGT 1046
Qy 315 ValValGluProAlaGly-----Arg 321
Db 1047 CTACTCCAAGAACCGGGTGGCCCTTGAAGAGGTGTCAAGACACTGAGGAGCAAG 1106
Qy 322 ProGly-SerProAlaProAlaGluLysValGluThrProSerProThrAlaSer--- 340
Db 1107 CCAGTATCAAGTCCCGAGATGAGGAGGTGTGGACGGGCCCTCGAACACAGCTCCCC 1166
Qy 340 ----- 340
Db 1167 TGCCCCCAGGTGTTCATGAACACAGCTGGACCGCATCAGCGAGGATGCGAGCCATGGGA 1226
Qy 341 -AlaLeuAspTyr-----ProSerGluAsnLeuAlaPheIleAspGluSe 355
Db 1227 CGCCCGAGGACTACCACTCATCTTCCAGGACGCCGACATCCTTCGTGGAACACGGA 1286
Qy 355 rSerAsp-ThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArg----- 371
Db 1287 GGCTGGCTCTCAGACAGGAGA-----CCTCAAGTCTCTGCTAGAGGACAA 1334
Qy 372 -----GlyArgArgProAsnProSerLysLysProSerArgPro 385
Db 1335 CTGGCAGGGAGGAGAGCCCGCCAGCGGGGCTGAAGCCAGGCGCCCC 1384

RESULT 12
US-09-561-763-6
; Sequence 6, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rofy A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; PRIOR FILING DATE: 2000-04-29
; PRIOR FILING DATE: 01-11-1999
; PRIOR FILING DATE: 01-11-1999
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (996)
US-09-561-763-6

Alignment Scores:
Pred. No.: 8,48e-25 Length: 996
Score: 427.50 Matches: 111
Percent Similarity: 51.79% Conservatives: 48
Best Local Similarity: 36.16% Mismatches: 115
Query Match: 20.56% Indels: 33
DB: 4 Gaps: 8

US-09-655-272-2 (1-398) x US-09-561-763-6 (1-996)
Qy 5 ThrLeuLeuAlaLeuLeuAlaLeuValLeuValSerGlyAlaLeuValPhe 24
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Db 64 ACCGTGCTCTGCTGCTGCGC-----TACCTGGCTTACCTGGCGTGGCCACCGCGGTGTTTC 120
Qy 25 GlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAspHisGlyArgAsp 44
Db 121 TGGACGCTGGAGGCGCGCGCGGCGAGGACTCCAGCGGAGCTTCAGCGCGGAGAGTGG 180
Qy 45 GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheLysLeu 64
Db 181 GAGCTGTGCAAGAACTTCAGCTGTCTGGACCGCGCGGCTGAGCTCGTGTATCCGGAT 240
Qy 65 LeuValGluAlaLeuGlyGlyAlaAenProGluThrSerTrpThrAsnSerAsn 84
Db 241 GTCGTCCAGCATACAAAACGAGGCC-----AGCCTCTCCAGCAACACACC 288
Qy 85 HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleThrThr 104
Db 289 AGCATGGGCGCTGGAGGCTCGTGGGCTCTCTCTTTCTGTGTCACCATCACC 348
Qy 105 IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124
Db 349 ATTGGCTATGGCAACCTGAGTGTGTACCAAGATGCTGCGGCTCTCTCTGCTCTTT 408
Qy 125 AlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGly 144
Db 409 GCCCTTGTGGGATCCCACTCAACCTCGTGGTCTC-----AACCGACTGGGG 456
Qy 145 SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164
Db 457 CATCTCATGACGAGGAGTAACCACTGGGCCAGCAGGCTGGGGGCGACCTGGCAGGAT 516
Qy 165 ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGlyCysLeuLeuPhe 184
Db 517 CCTGACAAGCGCGGTGGTGGCGGCTCTGGCGGCTCTCTCTCGGCGCTCTCTGCTCTTC 576
Qy 185 ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204
Db 577 CTGCTCTGCCACCGCTGTCTCTCCACATGGAGGCTGGAGCTTACACAGAGGCGTTC 636
Qy 205 TyrPheValIleValThrLeuThrValGlyPheGlyAspTyrValProGlyAspGly 224
Db 637 TACTTGGCTTATCATCCCTCAGCAGCTGGGCTTGGGCGACTTACGTGATTGGAATGAAC 696
Qy 225 ThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrpLeuPheGly 243
Db 697 CCTCCACAGAGGTACCCACTGTGTGTACAAAGATGCTGCTGCTGCTGCTCTTTGGG 756
Qy 244 LeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArg 263
Db 757 ATGGCATGGCTGGCTGTGATCATCAAACTCATCTCTCCAGCTGGAGAGCGCCAGGAGG 816
Qy 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276
Db 817 GTATGTTCTGTCGCCACCACTCTAGGAAGACTTC-----AGTCC 861
Qy 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296
Db 862 CAAAGCTGG-----AGACAGGAGGACCTGACCGG--- 888
Qy 297 ProProGluLysGluGlnPro 303
Db 889 GAGCCAGAGTCCCACTCCCA 909
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## RESULT 13

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US-09-431-367B-6
; Sequence 6, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MXI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
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; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
US-09-431-367B-6

Alignment Scores:      8.48e-25      Length:      996
Pred. No.:            427.50          Matches:    111
Score:                51.79%          Conservative: 48
Percent Similarity:   36.16%          Mismatches: 115
Best Local Similarity: 20.56%          Indels:     33
Query Match:         4
DB:                  Gaps:           8

US-09-655-272-2 (1-398) x US-09-431-367B-6 (1-996)
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Qy 5 ThrLeuLeuAlaLeuLeuAlaLeuValLeuTyrLeuValSerGlyAlaLeuValPhe 24
Db 64 ACCGTGCTCTGCTGCTGCTGCGC---TACCTGGCTTACCTGGCGTGGCCACCGCGGTGTTTC 120
Qy 25 GlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAspHisGlyArgAsp 44
Db 121 TGGACGCTGGAGGCGCGCGCGGCGAGGACTCCAGCGGAGCTTCAGCGCGGAGAGTGG 180
Qy 45 GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheLysLeu 64
Db 181 GAGCTGTTCAGAACTTCAGCTGTCTGGACCGCGCGGCTGAGCTCGTGTATCCGGAT 240
Qy 65 LeuValGluAlaLeuGlyGlyAlaAenProGluThrSerTrpThrAsnSerAsn 84
Db 241 GTCGTCCAGCATACAAAACGAGGCC-----AGCCTCTCCAGCAACACACC 288
Qy 85 HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleThrThr 104
Db 289 AGCATGGGCGCTGGAGGCTCGTGGGCTCTCTCTTTCTGTGTCACCATCACC 348
Qy 105 IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124
Db 349 ATTGGCTATGGCAACCTGAGTGTGTACCAAGATGCTGCGGCTCTCTCTGCTCTTT 408
Qy 125 AlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGly 144
Db 409 GCCCTTGTGGGATCCCACTCAACCTCGTGGTCTC-----AACCGACTGGGG 456
Qy 145 SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164
Db 457 CATCTCATGACGAGGAGTAACCACTGGGCCAGCAGGCTGGGGGCGACCTGGCAGGAT 516
Qy 165 ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGlyCysLeuLeuPhe 184
Db 517 CCTGACAAGCGCGGTGGTGGCGGCTCTGGCGGCTCTCTCTCGGCGCTCTCTGCTCTTC 576
Qy 185 ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204
Db 577 CTGCTCTGCCACCGCTGTCTCTCCACATGGAGGCTGGAGCTTACACAGAGGCGTTC 636
Qy 205 TyrPheValIleValThrLeuThrValGlyPheGlyAspTyrValProGlyAspGly 224
Db 637 TACTTGGCTTATCATCCCTCAGCAGCTGGGCTTGGGCGACTTACGTGATTGGAATGAAC 696
Qy 225 ThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrpLeuPheGly 243
Db 697 CCTCCACAGAGGTACCCACTGTGTGTACAAAGATGCTGCTGCTGCTGCTCTTTGGG 756
Qy 244 LeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArg 263
Db 757 ATGGCATGGCTGGCTGTGATCATCAAACTCATCTCTCCAGCTGGAGAGCGCCAGGAGG 816
Qy 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276
Db 817 GTATGTTCTGTCGCCACCACTCTAGGAAGACTTC-----AGTCC 861
Qy 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296
Db 862 CAAAGCTGG-----AGACAGGAGGACCTGACCGG--- 888
Qy 297 ProProGluLysGluGlnPro 303
Db 889 GAGCCAGAGTCCCACTCCCA 909
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Thu Feb 3 07:31:01 2005

Db 757 ATGGCATGGCTGGCTTGATCATCAAACTCATCTCTCCAGCTGGAGACGCCAGGAGG 816  
 QY 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276  
 Db 817 GATGTTCTCTGGCCACACAGCTCTAAGGAAGACTTC-----AAGTCC 861  
 QY 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296  
 Db 862 CAAAGCTGG-----AGACAGGGACCTGACCGG--- 888  
 QY 297 ProProGluLysGluGlnPro 303  
 Db 889 GAGCCAGAGTCCCACTCCCA 909

## RESULT 14

US-09-561-763-4  
 ; Sequence 4, Application US/09561763  
 ; Patent No. 6664373  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J. et al.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP2  
 ; CURRENT APPLICATION NUMBER: US/09/561,763  
 ; CURRENT FILING DATE: 2000-04-29  
 ; PRIOR FILING DATE: 01-11-1999  
 ; PRIOR APPLICATION NUMBER: US 09/259,951  
 ; PRIOR FILING DATE: 01-03-1999  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (122)..(1117)  
 US-09-561-763-4

Alignment Scores:  
 Pred. No.: 1.63e-24 Length: 1575  
 Score: 427.50 Matches: 111  
 Percent Similarity: 51.79% Conservative: 48  
 Best Local Similarity: 36.16% Mismatches: 115  
 Query Match: 20.56% Indels: 33  
 DB: 4 Gaps: 8

US-09-655-272-2 (1-398) x US-09-561-763-4 (1-1575)

QY 5 ThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuValSerGlyAlaLeuValPhe 24  
 Db 185 ACCGTGCTCTCTCTCTGCCC---TACCTGGCTTACCTGGCGTGGCCACCGGCTGCTC 241  
 QY 25 GlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAspHisGlyArgAsp 44  
 Db 242 TGGACGCTGGAGCGCGCGCGCGCGGAGGACTCCAGCGCGCTTCCAGCGCGCAAGTGG 301  
 QY 45 GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeu 64  
 Db 302 GAGCTGTTCGAACATTCACGTGTCTGGACCCCGCGCTGGACTCGCTGATCCGGAT 361  
 QY 65 LeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThrAsnSerSerAsn 84  
 Db 362 GTCTGTCAGCATACAAAAACGAGCC-----AGCCTCTCCAGCAACACCAACC 409  
 QY 85 HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleThrThr 104  
 Db 410 AGCATGGCGGCTGGGAGCTCGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 469  
 QY 105 IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124  
 Db 470 ATTGGCTATGGCACTGAGCCCCACACAGATGGCTGCGCGCTCTCTCTGCACTCTCTT 529

QY 125 AlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGly 144  
 Db 530 GCCCTTGTGGGATCCCACTCAACCTCGTGGTCTC-----AACCGATGGGG 577  
 QY 145 SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164  
 Db 578 CATCTCATGACGAGGAGTAACCACTGGGCCAGCAGGCTGGGGGACCTGGCAGGAT 637  
 QY 165 ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGlyCysLeuLeuPhe 184  
 Db 638 CCTGACAAAGCGCGGTGGCTGGCGGGCTCTGGCGCCCTCTCTCGGCGCTCTCTCTCTTC 697  
 QY 185 ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204  
 Db 698 CTGCTGCTGCACCGCTCTCTCTCCACATGAGGGCTGGAGCTACACAGAGGGCTTC 757  
 QY 205 TyrPheValIleValThrLeuThrThrValGlyPheGlyAspTrpValProGlyAspGly 224  
 Db 758 TACTTCGCTTCATCACCTCAGCACCGTGGCTTCGGCGACTACGCTGATGGATGAATGAAC 817  
 QY 225 ThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrpIleLeuPheGly 243  
 Db 818 CCCTCCAGAGGTACCCCACTGTGTCAAGAACATGCTGCTCTCTCTCTCTCTCTCTCTCT 877  
 QY 244 LeuAlaTrpPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArg 263  
 Db 878 ATGCATGGCTGGCTTGTATCATCAACTCATCTCTCCAGCTGGAGCCGACGAGGAGG 937  
 QY 264 -----ArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAla 276  
 Db 938 GTATGTTCTCTGCTGCCACACAGCTCTAAGGAAGACTTC-----AAGTCC 982  
 QY 277 AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296  
 Db 983 CAAAGCTGG-----AGACAGGGACCTGACCGG--- 1009  
 QY 297 ProProGluLysGluGlnPro 303  
 Db 1010 GAGCCAGAGTCCCACTCCCA 1030

## RESULT 15

US-09-431-367B-4  
 ; Sequence 4, Application US/09431367B  
 ; Patent No. 6670149  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP  
 ; CURRENT APPLICATION NUMBER: US/09/431,367B  
 ; CURRENT FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: 09/259,951  
 ; PRIOR FILING DATE: 1999-03-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1575  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (122)..(1117)  
 US-09-431-367B-4

Alignment Scores:  
 Pred. No.: 1.63e-24 Length: 1575  
 Score: 427.50 Matches: 111  
 Percent Similarity: 51.79% Conservative: 48  
 Best Local Similarity: 36.16% Mismatches: 115  
 Query Match: 20.56% Indels: 33  
 DB: 4 Gaps: 8

US-09-655-272-2 (1-398) x US-09-431-367B-4 (1-1575)

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QY      5  ThrLeuLeuAlaLeuLeuValLeuLeuTyrLeuValSerGlyAlaLeuValPhe 24
Db      |||:|||||
185  ACCGTGCTGCTGCTGCGC---TACCTGGCTTACCTGGCGTGGGCACCGCGCTGTTTC 241
QY      25  GlnAlaLeuGlnProHisGlnGlnAlaGlnLysMetAspHisGlyArgAsp 44
Db      |||:|||||
242  TGGACGCTGGAGCGCGCGCGGAGGACTCCAGCGCAGCTTCAGCGCGGACAAGTGG 301
QY      45  GlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAspPheIleLysLeu 64
Db      |||:|||||
302  GAGCTGTTGCAGAACTTCAGCTGCTGGACCGCGCGCTGGACTCGCTGATCCGGGAT 361
QY      65  LeuValGlnAlaLeuGlyGlyAlaAsnProGluThrSerTrpThrAsnSerSerAsn 84
Db      |||:|||||
362  GTGCTCAAGCATACAAAACGGAGCC-----AGCCTCTCTCAGCAACACCACC 409
QY      85  HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleIleThrThr 104
Db      |||:|||||
410  AGCATGGGGCGCTGGAGCTCGTGGGCTCTTCTTTCTGTGTCCACCATCACACC 469
QY      105  IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr 124
Db      |||:|||||
470  ATTGGCTATGGCAACCTGAGCCCCAACACGATGGCTGCCGCCCTCTTCGCACTCTTCT 529
QY      125  AlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAspArgLeuGly 144
Db      |||:|||||
530  GCCCTTGTGGGATCCCACTCAACCTCGTGGTCTC-----AACCAGCTGGGG 577
QY      145  SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrpHisValPro 164
Db      |||:|||||
578  CATCTCATGACGAGGAGTAACCACTGGCGCCAGCAGCGCTGGGGGGCACCTGGCAGGAT 637
QY      165  ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGlyCysLeuLeuPhe 184
Db      |||:|||||
638  CCTGACAGCGCGGTGGCTGGCGGCTCTGGCGCCCTCTCTCGGGCCCTCTGCTCTTC 697
QY      185  ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle 204
Db      |||:|||||
698  CTGCTGCTGCCACCGCTGCTCTTCTCCACATGGAGGGCTGGAGCTACACAGAGGGCTTC 757
QY      205  TyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrValProGlyAspGly 224
Db      |||:|||||
758  TACTTCGCTTCAACCCCTCAGCACCGTGGGCTTCGGGACTACGCTGATTGGAATGAAC 817
QY      225  ThrGlyGlnAsnSerProAla---TyrGlnProLeuValTrpPheTrpIleLeuPheGly 243
Db      |||:|||||
818  CCCTCCAGAGGTACCCACTGTGTGTACAGAACATGGTGTCCCTGTGGATCCTCTTTGG 877
QY      244  LeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArg 263
Db      |||:|||||
878  ATGGCATGGCTGGCCCTTGATCATCAAACTCATCTCTCCAGCTGGAGAGCCGAGGAGG 937
QY      264  -----ArgThrArgAlaGluMetGlyLeuThrAlaGlnAla 276
Db      |||:|||||
938  GTATGTTCTGTGCCACCACTCTAAGGAAGACTTC-----AAGTCC 982
QY      277  AlaSerTrpThrGlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaPro 296
Db      |||:|||||
983  CAAAGCTGG-----AGACAGGGACCTGACCGG--- 1009
QY      297  ProProGluLysGluGlnPro 303
Db      |||:|||||
1010  GAGCCAGAGTCCCACTCCCA 1030
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GenCore version 5.1.6  
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Run on: February 3, 2005, 01:34:36 ; Search time 697.536 Seconds  
(without alignments)  
3278.486 Million cell updates/sec

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Perfect score: 2079  
Sequence: 1 MRSTTLALLALLVLLVSG.....SKPSRPRGRLDRKAVPV 398

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Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
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18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
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20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result, No.	Score	Query Match	Length	DB ID	Description
1	1692.5	81.4	1182	14	US-10-243-035-1
2	1692.5	81.4	1257	9	US-09-828-035-3
3	1692.5	81.4	1257	15	US-10-146-733-30
4	1692.5	81.4	1260	15	US-10-345-680-45
5	1692.5	81.4	1260	15	US-10-391-399-20
6	1692.5	81.4	1408	9	US-09-828-035-1
7	1692.5	81.4	1408	15	US-10-146-733-28
8	1692.5	81.4	1408	15	US-10-352-684A-7
9	1692.5	81.4	1408	15	US-10-391-399-18
10	1692.5	81.4	2747	18	US-10-768-158-11
11	1692.5	81.4	2772	15	US-10-345-680-43
12	1688.5	81.2	3945	9	US-09-747-835A-30
13	1688.5	81.2	3945	16	US-10-312-312-30
14	1688.5	81.2	3996	9	US-09-747-835A-28
15	1688.5	81.2	3996	15	US-10-037-270-195
16	1688.5	81.2	3996	15	US-10-117-722-185
17	1688.5	81.2	3996	16	US-10-312-312-28
18	1688.5	81.2	3996	16	US-10-276-774-1249
19	812	39.1	1614	11	US-09-892-360-1
20	812	39.1	1632	10	US-09-852-386-34
21	812	39.1	1644	15	US-10-332-175-1
22	812	39.1	2028	16	US-10-262-511-105
23	812	39.1	2065	9	US-09-729-920-1
24	812	39.1	2065	18	US-10-887-932-1
25	812	39.1	2730	16	US-10-302-172-432
26	784	37.7	1994	9	US-09-828-746-5
27	778	37.4	1246	9	US-09-828-746-1
28	778	37.4	2391	18	US-10-349-528-9
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32	562	27.0	504	13	US-10-027-632-42355
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38	561	27.0	406	14	US-10-243-035-15
39	532.5	25.6	2351	16	US-10-459-190-3
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44	490	23.6	882	13	US-10-121-966-3
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ALIGNMENTS

RESULT 1  
US-10-243-035-1  
; Sequence 1, Application US/10243035  
; Publication No. US20030049697A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LESAGE, FLORIAN  
; APPLICANT: MAINGRET, FRANCOIS  
; TITLE OF INVENTION: NEW FAMILY OF MECHANOSENSITIVE HUMAN POTASSIUM CHANNELS  
; FILE REFERENCE: 1317-02  
; CURRENT FILING DATE: 2002-09-13  
; CURRENT APPLICATION NUMBER: US/10/243,035  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1182  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS

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; LOCATION: (1)...(1179)
US-10-243-035-1

Alignment Scores:
Pred. No.: 3.24e-142 Length: 1182
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 14 Gaps: 2

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QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
DB 61 GCCTGTGTTCGGGGCCCTGGAGCAGCCACGAGCAGCAGCCAGAGGGAGCTGGGG 120
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 121 GAGTCCGAGAGAGTTCTTGGAGGCCCATCCGTGTGTGAGCAGCAGGAGCTGGGCC 180
QY 61 PheileLysLeuLeuValGluAlaLeuGlyGlyAlaLeuValLeuValSerThrTrpThr 80
DB 181 CTCTATCAAGAGGTGGCTGATGCCCTGGAGGGGTGGGAGCCAGCAGAACCACTCGACC 240
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
DB 241 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGCGAGCGCTTCTTTTCTCAGGGACC 297
QY 101 IleileThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
DB 298 ATCATCATCCACCATCGCTATGGCAATGTGGCCCTGGCCACAGATGCCGGCGGCTCTTC 357
QY 121 CysilePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
DB 358 TGCACTCTTTATGGCTGGTGGGATTCGGCTGTTGGATCTTCTTGGCAGGGTGGG 417
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
DB 418 GACCGGTGGGCTCTCCCTGGCCATGGCATCGCTCACATTTGAAGCATCTTCTTGAAG 477
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGly 180
DB 478 TGGCAGCTGCCACCGAGCTAGTAAGAGTGTCTGGCGAGTGTCTTCTTCTGCTGATCGGC 537
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
DB 538 TGCCTGCTCTTGTCTTCCACGCCCATCGTTCGTGTTCTGTATATGGAGGACTGGAGCAAG 597
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
DB 598 CTGGAGGCCATCTACTTTGTCTATAGTACGCTTACCACCGGTGGCTTTGGCGACTATGTG 657
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTyrPheTrpIle 240
DB 658 GCGGCGCGGAGCCCGAGCAGATCCCGGCCCTATCAGCCGCTGGTGTGTCTGTATC 717
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
DB 718 CTGCTGCGCCCTTACTTCTCCCTCAGTGTCTACCAACCATCGGAACTGGCTCGAGTA 777
QY 261 ValSerArgArgThrArgAlaGluMetClyGlyLeuThrAlaGlnAlaSerTrpThr 280
DB 778 GTGTCCCGCCGACTCTGGGGCAGAGATGGCGGCGCTCAGGCTCAGGCTGCCAGCTGGACT 837
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
DB 838 GGCACAGTGAACGCGCGGTGACCCAGGAGCGCGGCGCGCGCGCGCGCGCGCGCGAGAG 897

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DB 946 AGGCCCGGATCCCTTTCGCCCGCCCGAGAGGCTCAGCCGCTTCCCGCCCGCAGGCTCG 1005
QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
DB 1006 GCCCTGGATTATCCAGCAGAGAACTGGCTTCATCAGCAGTCTTCGATACGCGAGC 1065
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
DB 1066 GAGCGGGCTGCCGCTGCCCGCGCGCGAGAGGTGCGCGCGCCCAAAATCCCGCCAGG 1125
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
DB 1126 AAGCCGCTGCGCGCGCGCGCGCGCGCGTCCCCGAGACAAAGGCGTGCCTGGT 1179

RESULT 2
US-09-828-035-3
; Sequence 3, Application US/09828035
; Patent No. US20020034781A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF
; FILE REFERENCE: MNI-142
; CURRENT APPLICATION NUMBER: US/09/828,035
; PRIORITY FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,734
; PRIORITY FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1257)
US-09-828-035-3

Alignment Scores:
Pred. No.: 3.5e-142 Length: 1257
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 9 Gaps: 2

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QY 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuValSerGly 20
DB 79 ATCGCAGCAGCAGCAGCTTCTGGCCCTGCTGGCGCTGCTGCTTACTTGGTGTCTGT 138
QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
DB 139 GCCTGTGTTCGGGGCCCTGGAGCAGCCACGAGCAGCAGCCAGAGGGAGCTGGGG 198
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
DB 199 GAGTCCGAGAGAGTTCTTGGAGGCCCATCCGTGTGTGAGCAGCAGGAGCTGGGCC 258
QY 61 PheileLysLeuLeuValGluAlaLeuGlyGlyAlaLeuValLeuValSerTrpThr 80
DB 259 CTCTATCAAGAGGTGGCTGATGCCCTGGAGGGGTGGGAGCCAGAACCACTCGACC 318
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
DB 319 AGCAACAGCAGCCAC---TCAGCCTGGGACCTGGGCGAGCGCTTCTTTTCTCAGGGACC 375

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121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db TGCATCTTTTATGCGCTGGTGGGATTCGCTGTTTGGGATCTTACTGGCAGGGGTCCGG 495  
141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db GACCGGCTGGGCTCTCCCTGCGCATGGTCATCGTACATTTGAAGCATCTTCTTGAAG 555  
161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180  
Db TGGCAGCTGCGCACCGGAGCTAGTAAGAGATGCTGTCGCGCATGCTTTTCTGCTGATCGC 615  
181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
Db TGCCTGCTCTTTGCTTCAGCCGACGTTGCTGCTTATGCTATGAGGACTGGAGCAAG 675  
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Db CTGGAGGCCATCTACTTTGTATGATGACGCTTACACCGTGGCTTTTGGCGACTATGTG 735  
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241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
Db CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGAACTGGCTGGAGTA 855  
261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280  
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281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300  
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301 GluGlnProLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320  
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321 ArgProGlySerProAlaProAlaGluValGlyValGlyValGlyProSerProThrAlaSer 340  
Db AGGCCCGATCCCTTCGCCCGCCCGGAGAGCTCAGCGCTTCCCGCGCCCGCGCTCG 1083  
341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
Db GCCTTGGATTATCCAGCAGAGAACCTGGCTTCATCGACGAGTCTCGGATACGACAGC 1143  
361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380  
Db GAGCGGCGCTGCGCGCTGCGCGCGCGCGCGGAGAGTGGCGCGCGCGCGCGCGCGG 1203  
381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398  
Db AGCCCGTGGCGG 1257

RESULT 3  
US-10-146-733-30  
; Sequence 30, Application US/10146733  
; Publication No. US20030165891A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Glucksmann, Maria A.  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
; TITLE OF INVENTION: HMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MNI-248  
; CURRENT APPLICATION NUMBER: US/10/146,733

; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 60/185,938  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/515,520  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/518,866  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: US 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: US 60/195,993  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: US 60/199,799  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/233,537  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: US 60/235,018  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US 60/235,059  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US 60/256,240  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/256,588  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/258,028  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: US 09/796,720  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 09/828,035  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 09/833,081  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 09/843,128  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: US 09/957,683  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: US 09/964,252  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 09/964,256  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 10/024,623  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1257)  
US-10-146-733-30

Alignment Scores:  
Pred. No.: 3,5e-142 Length: 1257  
Score: 1692.50 Matches: 328  
Percent Similarity: 88.44% Conservative: 24  
Best Local Similarity: 82.41% Mismatches: 41  
Query Match: 81.41% Indels: 5  
DB: 15 Gaps: 2

US-09-655-272-2 (1-398) x US-10-146-733-30 (1-1257)

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QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40  
Db 139 GCCTCGTGTTCGGGCGCTTGGAGCAGCCGCCAGCAGCAGCGAGGAGTGGGG 198  
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
Db 199 GAGGTCCGAGAGAAGTTCTCTGAGGGCCCATCCGTGTGTGAGCGCAGCGAGCTGGGCTC 258



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QY 121 CysilePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 436 TGCATCTTCTATGCGCTGGTGGGATTCGCTGTTTGGATCTTACTGGCAGGGTGGG 495
QY 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 496 GACCGGCTGGGCTCCCTCCCTGCGCCATGGGATCGGTACATTAAGGCCATCTTCTTGAAG 555
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 556 TGCACGTGACCGGAGCTAGTAGAGTCTGTGCGGATGTTTCTGCTGATCGGC 615
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 616 TGCCTGCTCTTGTCTCTACCGCCACGCTTCTGCTATATGAGGACTGGAGCAAG 675
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 676 CTGGAGGCCATCTACTTGTGATAGTACGCTTACCACCGTGGGCTTGGCGACTATGTG 735
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTyrPheTrpIle 240
Db 736 GCCGGCGGACCCGAGGAGTCTCCCGGCTATCAGCGCTGTGTGGTCTGTGATC 795
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 796 CTGCTCGGCTGCTTACTTCTGCTCAGTGTCTACCACTCGGAACCTGGCTGCGAGTA 855
QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaSerTrpThr 280
Db 856 GTGTCGCGCGCATCTCGGCGAGAGTGGCGGCTCTCAGGCTCAGGCTGCGAGT 915
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 916 GGCACAGTGAAGCGCGTGACCCAGCAGCGCGGCCCGCCCGCCCGCGGAGAG 975
QY 301 GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320
Db 976 GAGCAGCCACTG-----CTGCTCCAGCGGCTCTCCAGCGAGCGCTGGGC 1023
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db 1024 AGGCCCGATCCCTTCCGCCCGCGAGAGGCTCAGTCTTCCCGCCCGCGGCTCG 1083
QY 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1084 GCCTTGATTTATCCAGCGAGAACCTGGCTTTCATCGACGAGTCTCGGATACGAGC 1143
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 1144 GAGCGGCTGCCGCTGCCCGCGCGCGAGAGTCCGCGCCCAATCCCGCCAGG 1203
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1204 AAGCCGTCGGCGCGCGCGCGCGTCCCGAGACAAAGCGCGTGGCGGTG 1257

RESULT 5
US-10-391-399-20
; Sequence 20, Application US/10391399
; Publication No. US20030219806A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Lora, Jose M.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,
; TITLE OF INVENTION: 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921
; TITLE OF INVENTION: AND 33751 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0200MIN
; CURRENT APPLICATION NUMBER: US/10/391.399
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; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/789,481
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 09/634,669
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 09/583,373
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/510,706
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 10/309,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/336,936
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 10/094,214
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US60/275,078
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1260)
; US-10-391-399-20

Alignment Scores:
Prod. No.: 3 51e-142 Length: 1260
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 15 Gaps: 2

US-09-655-272-2 (1-398) x US-10-391-399-20 (1-1260)
QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20
Db 79 ATGCGCAGCACACGCTCTGCGCCCTGCTGGCGCTGCTTGTCTTACTTGGTCTGCT 138
QY 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysMetAsp 40
Db 139 GCCTGTGTGTTCCGGCCCTTGGAGCAGCCGCCACGAGCAGCAGCGAGGGAGCTGGG 198
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 199 GAGGTCCGAGAGAAGTTCTTGAGGGCCCATCCGTGTGTGAGCCACGAGAGCTGGGCTC 258
QY 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 259 CTCATCAGGAGGTGGCTGATGCCCTGGGAGGGGTGGGACCCAGAACCACTCGACC 318
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 319 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGAGCGCTTCTTTTCTCAGGACC 375
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyAspLeuPhe 120
Db 376 ATCATCACCACCATCGGCTATGGCAATGGCCCTGGGCACACATGCCGGGCCCTCTTC 435
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 436 TGCATCTTATGCGCTGGTGGGATTCGCTGTTTGGGATCTTACTTGGCAGGGTGGG 495
QY 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
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496	GACCGCTGGCTCCTCCCTCGCGCATGGCATCGGTGCACATTGAAGCCATCTTCTTGAAG	555
161	TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly	180
556	TGGCAGCTGCCACCGGAGCTAGTAAGAGTGCTGTGGGATGCTCTTTCTGCTGATCGGC	615
181	CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys	200
616	TGCTGCTCTTGTCTCCTCAGCCACGTTTCGTGTTCTGCTATATGGAGACTTGGAGCAAG	675
201	LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal	220
676	CTGGAGCCCATCTACTTTGTTCATAGTAGAGCTTACCACCGTGGCTTGGCGACTATGTG	735
221	ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle	240
736	GCCGGCGGAGCCCGCAGGACTCCCGGCCCTATCAGCCGTGGTGTGGTCTTGGATC	795
241	LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla	260
796	CTGCTCGCCTGGCTTACTTTCGCTCAGTGCTCACCACATCGGAACTGGCTGGCAGTA	855
261	ValSerArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaSerTrpThr	280
856	GTGTCCCGCCCATCTCGGCAGAGATGGCGGCTCAGCGCTCAGCGTGCAGCTGGACT	915
281	GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys	300
916	GGCAGTGTACAGCGCGCTGACCACGAGCGGGCCCGCCGCCCGCCGCGAGAG	975
301	GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValGluProAlaGly	320
976	GAGCAGCCACTG-----CTGCCTCCACCGCCCTGTCTCAGCGCAGCGCTGGGC	1023
321	ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer	340
1024	AGGCCCGCATCCCTTCGCCCGCCGAGAGGCTCAGCGCGCTTCCCCGCCACCGGCTCG	1083
341	AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer	360
1084	GCCTTGGATTATCCGACGGAGAACCTTGGCTTCATCGACGAGTCTCTCGGATACGCAGGC	1143
361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys	380
1144	GAGCGGGCTGCGCGTGCCTCGCGCGCGGAGAGTCCCGCCGCCCAATATCCCCCAGG	1203
381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398
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RESULT 6  
US-09-828-035-1  
; Sequence 1, Application US/09828035  
; Patent No. US20020034781A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria A.  
; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF  
; FILE REFERENCE: MNI-142  
; CURRENT APPLICATION NUMBER: US/09/828,035  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1408  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (84) ..(1340)  
US-09-828-035-1

Alignment Scores:	4.02e-142	Length:	1408
Pred. No.:	1692.50	Matches:	328
Score:	88.44%	Conservative:	24
Percent Similarity:	82.41%	Mismatches:	41
Best Local Similarity:	81.41%	Indels:	5
Query Match:	9	Gaps:	2
DB:			
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Qy	1	MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuValSerGly	20
Db	162	ATGCGCAGCACCACGCTCTGGCCCTGCTGGCGTGGTCTTCTTACTTGGTCTGGT	221
Qy	21	AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysMetAsp	40
Db	222	GCCTCGGTTCGCGCCCTGGAGCAGCCCCACAGCAGCAGCGCCAGAGGAGCTGGG	281
Qy	41	HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp	60
Db	282	GAGTCCGAGAGAAGTTCCTGAGGGCCCATCGTGTGTGAGCGACCGAGCTGGGCTC	341
Qy	61	PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr	80
Db	342	CTCATCAGAGGTGGCTGATGCCCTGGAGGGGGTGGCGGCCAGAACCACTCGACC	401
Qy	81	AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr	100
Db	402	AGCAACAGCAGCCAC--TCAGCTGGGACCTGGGCAGCGCTCTCTTTCTCAGGGACC	458
Qy	101	IleIleThrThrIleGlyTyrglyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe	120
Db	459	ATCATCACCACTCGGCTATGCGCAATGGCCATGGCCCTCGCCACAGATCGCGGGCTCTTC	518
Qy	121	CysIlePheTyrrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly	140
Db	519	TGCATCTTTATGGCGTGGTGGGATTCGCTGTTTGGGATCTACTTGCAGGGTCCGG	578
Qy	141	AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys	160
Db	579	GACCGCTGGGCTCCTCCCTCGCCCATGGGCATCGGTCACTTGAAGCCATCTTCTGAAG	638
Qy	161	TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly	180
Db	639	TGGCAGTGGCCACCGAGCTATGAGAGTCTCTCGCGCATGCTTTCTCTGCTGATCGGC	698
Qy	181	CysLeuLeuPheValLeuThrProThrPheValPheSerTyrrMetGluSerTrpSerLys	200
Db	699	TGCTGCTCTTTGCTCTCAGCCACCTGCTGTGTTCTGTATATGAGGAGCTGGAGCAAG	758
Qy	201	LeuGluAlaIleTyrrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrrVal	220
Db	759	CTGGAGGCCATCTACTTTGTATAGTGACCTTACCACTGGGCTTGGCGACTATGTG	818
Qy	221	ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrrGlnProLeuValTrpPheTrpIle	240
Db	819	GCGCGCGCGGACCCAGCAGGAGCTCCCGGCCCTATCAGCGCTGTGTGTGTCTGGATC	878
Qy	241	LeuPheGlyLeuAlaTyrrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla	260
Db	879	CTGCTCGGCTGGCTTACTTGGCTCTAGTGTCTACCACTACCGGCTCAGGCTGCAGCTG	938
Qy	261	ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaLaSerTrpThr	280
Db	939	GTGTCCCGCGCAGCTCGGCAGAGATGGCGGCCCTCAGGCTCAGGCTGCAGCTGAGCT	998
Qy	281	GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys	300
Db	999	GGCACAGTGACAGCGCGCTGACCCAGGAGCGCGGCCCGCCCGCCCGCGAGAG	1058
Qy	301	GluGlnProLeuLeuProSerSerProAlaProAlaValValGluProAlaGly	320
Db	1059	GAGCAGCAGCTG-----CTGCCCTCAGCGCCCTGTCCAGCGCAGCGCTGGC	1106

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QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db 1107 AGCCCCGATCCCTTCGCCGCCCGAGAGAGCTCAGCGCGCTTCCCGCCCGCCACGGCTCG 1166
QY 341 AlaLeuAspTyrProSerGluAenLeuAlaPheAlaAspGluSerSerAspThrGlnSer 360
Db 1167 GCCTTGATATTATCCAGCGAGAACCTGGCCTTCATCGACAGTCTCTGGATACGCAGAGC 1226
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAenProSerLys 380
Db 1227 GAGCGCGCTGCCGCTGCCCGCGCGCGAGAGTCCGCGCGCCCAATCCCGCCAGG 1286
QY 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1287 AAGCCCGTGGCGCGCGCGCGCGCGTCCCGGAGACAAAGCGTGGCGGTG 1340
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## RESULT 7

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US-10-146-733-28
; Sequence 28, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 28
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)..(1340)
US-10-146-733-28

Alignment Scores:
Pred. No.: 4,02e-142 Length: 1408
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 2 Gaps: 2

US-09-655-272-2 (1-398) x US-10-146-733-28 (1-1408)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20
Db 162 ATGCGCAGCACACAGCTCTGCGCCCTGCTGGCGCTGCTTGTCTTACCTGTGTGTGT 221
QY 21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnAlaGlnLysLysMetAsp 40
Db 222 GCGCTGTGTTCGGGCGCCCTGGAGCAGCCCGCAGCAGCAGCGCCGAGGAGTGGGG 281
QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 282 GAGGTCCGAGAGAGTTCTTGAAGGCCCATCGTGTGTGAGCAGCAGGAGCTGGGCTC 341
QY 61 PheLeuLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 342 CTCATCAAGGAGGTGGCTGATGCTTGGGAGGGGTGGGACCCAGAAACCACTCGACC 401
QY 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr 100
Db 402 AGCACAGCAGGCGCAC---TCAGCCTGGGACCTGGGCGAGCGCTCTCTTTCTCAGGACC 458
QY 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 459 ATCATCACCACCATCGGCTATGGCAATGGCCCTGCGGCACAGATGCCGGGCGCTCTTC 518
QY 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 519 TGCATCTTTATGCGCTGTGGGATTCCGCTGTTGGGATCCTACTGGCAGGGGTGGGG 578
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 579 GACCGGCTGGGCTCTCTCCCTGCGCCCATGGCATGGTCACTTGAAGCCATCTTCTTGAAG 638
QY 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 639 TGGCAGTCCGACCGGAGGTAGTAGAGTGTGTGCGCGATGCTTTTCTGCTGATCGGC 698
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 699 TGCCTGCTCTTTGTCTCTACGCCACCGTTCGTGTTCTGCTATATGAGGAGCTGAGCAAG 758
QY 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220
Db 759 CTGGAGGCCATCTACTTTGTTCATAGTACGCTTACCACCGCTGGGCTTTGGCGCATGTG 818
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 819 GCGGCGCGGACCCGAGGAGGACTCCCCGGCCCTATCAGCCGCTGTGTGTGTGTGTGATC 878
QY 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 879 CTGCTCGGCTGGCTTACTTTCGCTCAGTGTCTCACCACCATCGGGAACCTGGCTCGCAGTA 938
QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaSerTrpThr 280
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Db 939 GTGTCCCGCCACTCGGCGAGAGATGGCGGCGCTCACGGCTCAGGCTGCCAGCTGGACT 998
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGCACGGCGTGTACCCAGCAGCGCGGCGCGCGCGCGCGGAGAAG 1058
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1059 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCGAGCGCGTGGGC 1106
Qy 321 ArgProGlySerProAlaProAlaGluValGluThrProSerProProThrAlaSer 340
Db 1107 AGGCCCGCATCCCTCGCCCGGAGAGCTCAGCGGCTTCCCGCCGCGCGGCTCG 1166
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1167 GCCCTGATATCCAGCGAGACCTGGCTTCATCGAGTCTCTCGGATACGAGAGC 1226
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgProAsnProSerLys 380
Db 1227 GAGCGCGCTGCCCGTCCCGCGCGCGCGAGAGGTGCGCGCGCCCAATCCCCCAGG 1286
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1287 AAGCCCGTGGCGCGCGCGCGCGCGCTCCCGAGACAAAGCGCTGCCGCTG 1340

RESULT 8
US-10-352-684A-7
; Sequence 7, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPT02-0191RNMNM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: (84)....(1343)
US-10-352-684A-7
Alignment Scores: 4.02e-142 Length: 1408
Pred. No.: 1692.50 Matches: 328
Score: 88.44% Conservative: 24
Percent Similarity: 82.41% Mismatches: 41
Best Local Similarity: 81.41% Indels: 5
Query Match: 15 Gaps: 2
DB:

US-09-655-272-2 (1-398) x US-10-352-684A-7 (1-1408)
Qy 1 MetArgSerThrThrLeuLeuAlaLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20
Db 162 ATGCGCAGCACCAGCTCTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 221
Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnGlnAlaGlnLysLysMetAsp 40
Db 222 GCCCTGTGTGTTCGGGCGCTGGAGCAGCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 281
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 282 GAGTCCGAGAGAGTTCCTGAGGGGCCATCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 341
Qy 61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 342 CTCATCAGAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 401
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr 100
Db 402 AGCAACAGCAGCCAC--TCAGCTCTGGGACCTGGGCGAGCGCTCTCTTTTCTCAGGGACC 458
Qy 101 IleIleThrThrIleGlyTyrGlyAsnLleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 459 ATCATCACCATCCGCTATGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 518
Qy 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 519 TGCATCTTTTATGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 578
Qy 141 AspArgLeuGlySerSerLeuArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 579 GACCGGCTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 638
Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 639 TGGCAGCTGCCACCGGAGCTAGTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 698
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 699 TGCCTGCTCTTTGTCTCTCACGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 758
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 759 CTGGAGGCCATCTACTTTGTCTAGTACGCTTACCGCGTGGGCTTTTGGCGACTATGTG 818
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 819 GCCGGCGCGGAGCCCGCAGGAGGACTCCCGGCGCTATCACCGCTGTGTGTGTGTGTGTGT 878
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 879 CTGCTCGGCTGTGCTTACTTCGCTCAGTGTCTCAGCCATCCAGCAGTGGGCTGGCGAGTA 938
Qy 261 ValSerThrArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 939 GTGTCCCGCGCACTCGGCGAGAGATGGCGGCGCTCACGGCTCAGGCTGCCAGCTGCACT 998
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGCACGGCGTGTACCCAGCAGCGCGGCGCGCGCGCGCGGAGAAG 1058

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Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1059 GAGCAGCCACTG-----CTGCCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 1106

Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db 1107 AGGCCCGCATCCCTTCGCCCGCAGAGAGCTCAGCGGCTTCCCGCCACGCGCTCG 1166

Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 1167 GCCTGTGATTATCCACGAGAACCTGCGCTTCATCAGCAGTCTCGGATACGAGAGC 1226

Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAnProSerLys 380
Db 1227 GAGCGCGGCTGCCCGCTGCCCGCGCGCGAGAGGTGCGCGCGCCCAAAATCCCCAGG 1286

Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal 398
Db 1287 AGCCCCGTGCGCCCCCGCGCGCGCGCGCTCCCGAGACAAAGCGTGCCGGTG 1340
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## RESULT 9

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US-10-391-399-18
; Sequence 18, Application US/10391399
; Publication No. US20030219806A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Lora, Jose M.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,
; TITLE OF INVENTION: 52920, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921
; TITLE OF INVENTION: AND 33751 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0200NM
; CURRENT APPLICATION NUMBER: US/10/391,399
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/789,481
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 09/634,669
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 09/583,373
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/510,706
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 10/309,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/336,936
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 10/094,214
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US60/275,078
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1343)
US-10-391-399-18
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Alignment Scores:
Pred. No.: 4,02e-142 Length: 1408
Score: 1692.50 Matches: 328
Percent Similarity: 88.44% Conservative: 24
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Best Local Similarity: 82.41% Mismatches: 41
Query Match: 81.41% Indels: 5
DB: 15 Gaps: 2
US-09-655-272-2 (1-398) x US-10-391-399-18 (1-1408)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20
Db 162 ATCGCAGCAGCAGCAGCTCTGGCCCTCTGGCGCTGTCTTGTCTTACTTGTGTCTGT 221

Qy 21 AlaLeuValPheGlnAlaLeuGluGlnProHisGluGlnAlaGlnLysLysMetAsp 40
Db 222 GCCTCGTGTTCGGGCCCTGGAGCAGCCCCACAGCAGCAGCAGCAGGAGCTGGGG 281

Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60
Db 282 GAGTCCGAGAGAGTTCCTGAGGGCCCATCCGTGTGTGAGCGACACGAGGCTGGGCC 341

Qy 61 PheIleLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 342 CTCATCAAGAGGTGGCTGATGCCCTGGGAGGGGTGCGGACCCAGAAACCACTCGACC 401

Qy 81 AsnSerSerAsnHisSerSerAlaTtpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 402 AGCAACAGCAGCCAC---TCAGCTGGGACCTGGGCGCGCTCTCTTTTCTCAGGACC 458

Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 459 ATCATCACCATCATCGCTATGGCAATGTGGCCCTGGCCACAGATGCCGGCGCCTTTC 518

Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 519 TGCATCTTTATGCGCTGTGGGATTCGCTGTTTGGGATCTTACTGGCAGGGCTGGG 578

Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 579 GACCGCTGGGCTCTCCCTGGCCCATGGCATCGGTCACTTGAAGCCATCTTCTTGAAG 638

Qy 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuGly 180
Db 639 TGGCAGCTGCCACCGGAGCTAGTAGAGTGTCTCGCGATGCTTTTCTGCTGATCGGC 698

Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200
Db 699 TGCCTGCTCTTTGCTCTCACGCCACCGTTCGTCTTATATGAGGACTGGAGCAAG 758

Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrValGlyPheGlyAspTyrVal 220
Db 759 CTGGAGGCCATCTACTTTGTATAGTACGCTTACCACCGTGGGCTTTGGCGACTATGTG 818

Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240
Db 819 GCCGGCGCGGACCCACGAGGAGCTCCCGGCTATCAGCGCTGTGTGTGTCTGATC 878

Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 879 CTGCTCGGCTGCTTACTTCGCTCAGTGTCTCACCACCATCGGAACCTGGCTGCGAGTA 938

Qy 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaIleSerTrpThr 280
Db 939 GTGTCCCGCGCAGCTCGGCGAGATGGGGCGGCTCAGCGCTCAGGCTGCGAGCTGACT 998

Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 999 GGCACAGTGCAGCGCGCTGACCCAGCAGCGCGCGCGCGCGCGCGCGCGGAGAG 1058

Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValValGluProAlaGly 320
Db 1059 GAGCAGCCACTG-----CTGCCTCCACCGCCCTGTCCAGCAGCAGCGCTGGGC 1106

Qy 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer 340
Db 1107 AGGCCCGCATCCCTTCGCCCGCAGAGAGGTGCGCGCGCCCAAAATCCCCAGG 1166
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	321	ArgProGlySerProAlaGluLysValGluThrProSerProProThrAlaSer	340
Qy			
		:::	:::
Db	1087	AGGCCCGATCCCTTTCGCCCGCAGGAAGGCCTCAGCTGCCTTCCCGCCACGGCCTCG	1146
Qy	341	AlaLeuAspTyrrProSerGluAnLeuAlaPheIleaspClusSerSerAspThrGlnSer	360
Db	1147	GCCCTGGATTATCCCAAGCAGAACTTCGTGGCTTCATCGACGAGTCTCTGGGATACGCACAGC	1206
Qy	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAenProSerLys	380
Db	1207	GAGCGCGGCTGCCCGTGCCCGCGCGCAGAGGTGCGCGCCCAAATCCCCCAGG	1266
Qy	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValProVal	398
Db	1267	AAGCCCGTGCGGCGCCCGCGCGCCCGCGGCTCCCGCGAGACAAAGGCGTGCCGGTG	1320

RESULT 12  
US-09-747-835A-30  
; Sequence 30, Application US/09747835A  
; Patent No. US2002014692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Asundi, Vinod



; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 30  
; LENGTH: 3945  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-312-312-30

Alignment Scores:  
Pred. No.: 3,27e-141 Length: 3945  
Score: 1688.50 Matches: 327  
Percent Similarity: 88.41% Conservatives: 24  
Best Local Similarity: 82.37% Mismatches: 41  
Query Match: 81.22% Indels: 5  
DB: 16 Gaps: 2

US-09-655-272-2 (1-398) x US-10-312-312-30 (1-3945)

Qy 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuValLeuValSerGly 20  
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Qy 21 AlaLeuValPheGlnAlaLeuGlnProHisGlnGlnAlaGlnLysLysMetAsp 40  
Db 1678 GCCTGTGTGTTCGGGCCCCCTGGAGACGCCACGAGCAGAGCCGCCAGAGGGAGCTGGGG 1737  
Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
Db 1738 GAGGTCCGAGAGAGTTCTTGGGGCCCATCGGTGTGTGAGCACCAGGAGCTGGGCCTC 1797  
Qy 61 PheIleLysLeuLeuValGlnAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
Db 1798 CTCATCAAGAGGTGGCTGATCCCTGGAGGGGGTGGCAGCCAGAAACCACTCGACC 1857  
Qy 81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
Db 1858 AGCAACAGCAGCCAC---TCAGGCTGGGACCTGGCAGCGCCCTTCTTTTCTCAGGACC 1914  
Qy 101 IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120  
Db 1915 ATCATCACCACTCGGCTATGGCATGTGGCCCTGGCAGACATGCCGGCGCCCTCTTC 1974  
Qy 121 CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140  
Db 1975 TGCATCTTTTATGCGCTGTGGGGATTCCGCTGTTTGGGATCCTACTGGCAGGGTGGG 2034  
Qy 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160  
Db 2035 GACCGGCTGGGCTCTCTCCCTGGCCCATGGCATCGGTACATTTGAAGCCATCTTCTTGAAG 2094  
Qy 161 TrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180  
Db 2095 TGGCAGTGCACCGAGCTAGTAAGAGTCTGTGGCGATGCTTTCTGCTGATCGGC 2154  
Qy 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys 200  
Db 2155 TGCCTGCTCTTCTCTCCACGCCACCGTTCGTGTCTGTATATGAGGAGCTGAGCAAG 2214  
Qy 201 LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal 220  
Db 2215 CTGGAGCCCATCTACTTTGTATAGTACGCTTACCACCGTGGCTTTGGCGACTATGTG 2274  
Qy 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle 240  
Db 2275 GCCGGCGGACCCCGAGGAGACTCCCGCGCCATACAGCCGCTGTGGTGTCTGATC 2334  
Qy 241 LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260  
Db 2335 CTGCTCGGCTGGCTACTTCTGCTCAGTGTCTCACCACCATCGGAACTGGCTGGCAGTA 2394  
Qy 261 ValSerArgArgThrArgAlaGluMetGlyLeuThrThrAlaGlnAlaSerTrpThr 280

Db 2395 GTGTCCCGCGCACTCGGCAGAGATGGGGCGCTTACGGCTCAGGCTGCGCTGACT 2454  
Qy 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProProGluLys 300  
Db 2455 GGCACAGTGCACGGCGGTGACCCAGAGAGCCGGCCCGCCCGCCCGCGGAGAG 2514  
Qy 301 GluGlnProLeuLeuProSerSerLeuProAlaProProAlaValGluProAlaGly 320  
Db 2515 GAGCAGCCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCTGGGC 2562  
Qy 321 ArgProGlySerProAlaProAlaGluValGluThrProSerProProThrAlaSer 340  
Db 2563 AGGCCCGGATCCCTTTCGCCCGCCGAGAGGCTCAGCGGCTTCCCGCCCGCAGCGCTCG 2622  
Qy 341 AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360  
Db 2623 GCCTGTGATATCCAGCGAGAACCTGGCTTCATCGAGAGTCTCGGATACGAGAGC 2682  
Qy 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380  
Db 2683 GAGCGGGGTGCGCGCTGCGCGCGCGAGAGGTGCGCGCGCCCAATCCGCCAGG 2742  
Qy 381 LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValPro 397  
Db 2743 AGCCCGTGGCG 2793

RESULT 14  
US-09-747-835A-28  
; Sequence 28, Application US/09747835A  
; Patent No. US2002014692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE  
; TITLE OF INVENTION: (LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-37CIP  
; CURRENT APPLICATION NUMBER: US/09/747,835A  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 09/729,739  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: US 09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 28  
; LENGTH: 3996  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (52)..(3996)  
US-09-747-835A-28

Alignment Scores:  
Pred. No.: 3,32e-141 Length: 3996  
Score: 1688.50 Matches: 327  
Percent Similarity: 88.41% Conservatives: 24

Best Local Similarity:	82.37%	Mismatches:	41
Query Match:	81.22%	Indels:	5
DR:	9	Gaps:	2

US-00-555-272-2 (1-398) x US-09-747-835A-28 (1-3996)

1	MetArgSerThrThrLeuLeuAlaLeuAlaLeuValLeuLeuValLeuValSerGly	20
1669	ATCGGCAGACCAAGCTCTGGCCCTGCTGGCGCTGGTCTTGTCTTATCTTGGTGTGGT	1728
21	AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysLysMetAsp	40
1729	GCCTCGTGTTCGGGCCCTTGAGCAGACCCACGACGACGAGCCACGAGGAGCTGGG	1788
41	HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuAlaAsp	60
1789	GAGTCCGAGAGAAGTTCCTGAGGGCCCATCGCTGTGTGAGCGACACGAGACTCGGCCTC	1848
61	PheIleLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr	80
1849	CTCATCAAGAGGTGGCTGATGCTCCCTGGGAGGGGTGGCGACCCAGAACCACTCGACC	1908
81	AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePhePheSerGlyThr	100
1909	AGCAACAGCAGCCAC---TCAGCTCGGACCTGGGCAGCGCCCTCTTTTCTCAGGGACC	1965
101	IleIleThrThrIleGlyTyrGlyAsnIleValLeuHisAspAlaGlyArgLeuPhe	120
1966	ATCATCACCAACATCGCTATGGCAATGTGGCCCTCGGCACAGATGCCGGGCGCTCTTC	2025
121	CysIlePheTyrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly	140
2026	TGCATCTTTTATCGCTGGTGGGATTCGCTTTGGGATCTCTACTGCGAGGGTCTGGG	2085
141	AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys	160
2086	GACCGGGCTGGGCTCTCTCCCTCGGCATGGCATCGGTACATGAAGCCATCTTCTGAAG	2145
161	TrpHisValProGlyIleValArgSerLeuSerAlaValLeuPheLeuLeuIleGly	180
2146	TGGCAGCTGCCACCGAGCTAGTAAGAGTGTGTGCGCGATGCTTTCTCTGTGATCGGC	2205
181	CysLeuLeuPheValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLys	200
2206	TGCTGTCTTTGTCTCTCAGCCACAGTTCGTGTCTGCTATATGGAGGACTGGAGCAAG	2265
201	LeuGluAlaIleTyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrVal	220
2266	CTGGAGGCCATCTACTTTGTCATAGTAGCGTTACCACCGTGGCTTTGGCGACTATGTG	2325
221	ProGlyAspGlyThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIle	240
2326	GCCGGCGCGGACCCACGAGGAGCTCCCGCGCCTATCAGCGCTGGTGTGGTCTCGATC	2385
241	LeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla	260
2386	CTGCTCGGCTGGCTTACTTCGCTCAGTGTCTACCACTCGGGAATGGCTGCGAGTA	2445
261	ValSerArgGThrArgAlaGluMetGlyLeuThrAlaGlnAlaAlaSerTrpThr	280
2446	GTGTCCCGCGCGACTCGGCAGAGATGGCGGCCCTCAGGCTCAGGCTGCCAGCTGACT	2505
281	GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys	300
2506	GGCACAGTGACGCGCGCTGACCCACGAGCGCGGCGCGCGCCGCCCGCCGAGAG	2565
301	GluGlnProLeuLeuProSerSerLeuProAlaProAlaValValGluProAlaGly	320
2566	GAGCAGCACTG-----CTGCTCCACCGCCCTGTCCAGCGCAGCGCGCTGGGC	2613
321	ArgProGlySerProAlaProAlaGluLysValGluThrProSerProProThrAlaSer	340
2614	AGGCCCGGATCCCTTTCGCCCCCGGAGAGGTCTCCGCCCTTCCCGCCGACGGCTCG	2673

QY	341	AlaLeuAspTyrProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer	360
Db	2674	GCCTCGGATTAATCCAGCGAGACCTGGCTTCAICGAGAGTCTCTCGATACGACAGC	2733
QY	361	GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgGlyArgArgProAsnProSerLys	380
Db	2734	GAGCGCGCTGCCCGCTGCCCCGCGCGCGAGAGTGTGCGCGCGCCCAATCCCCCCAGG	2793
QY	381	LysProSerArgProArgGlyProGlyArgLeuArgAspLysAlaValPro	397
Db	2794	AAGCCGTGCGGCCCGCGGCCCGCGCGTCCCGCGAGACAAAGGCGTGCCCG	2844

## RESULT 15

US-10-037-270-195  
; Sequence 195, Application US/10037270  
; Publication No. US20030104529A1

```

GENERAL INFORMATION:
APPLICANT: Tang, Yi. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyang
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A..
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 195_
LENGTH: 3996
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3996)
US-10-037-270-195

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Alignment Scores:	3 32e-141	Length:	3996
Pred. No.:	1688 50	Matches:	327
Score:	88.41%	Conservative:	24
Percent Similarity:	82.37%	Mismatches:	41
Best Local Similarity:	81.22%	Indels:	5
Query Match:	15	Gaps:	2
Dn:			

--- 22 255 070 0 (1 398) ~ 119-10-037-270-195 (1-3996)

QY	1	Met	Arg	Ser	Thr	Thr	Leu	Leu	Ala	Leu	Ala	Leu	Val	Leu	Leu	Val	Ser	Gly	20	
DB	1669	AT	CG	CA	GAC	CA	CG	CT	CG	CC	TG	CG	CG	GT	GC	TC	TT	CT	1728	
QY	21	Ala	Leu	Val	Phe	Gln	Ala	Leu	Glu	Gln	Pro	His	Glu	Gln	Ala	Gln	Lys	Met	Asp	40
DB	1729	GC	CT	TG	TG	T	TC	CG	GC	CC	CT	CG	AG	CA	CG	CC	CA	GAG	CT	1788

Search completed: February 3, 2005, 06:54:04  
Job time : 711.536 secs

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QY 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnIlySerLeuGluAsp 60
Db 1789 GAGGTCCGAGAGAAGTTCCTGAGGGCCCATCCGTGTGTGAGGACACGAGGCTGGGCCTC 1848
QY 61 PheIleLeuLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80
Db 1849 CTCATCAGGAGGTGGCTGATGCCCTGGAGGGGGTGGGACCCAGAAACCACTCGACC 1908
QY 81 AsnSerSerAsnHisSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100
Db 1909 AGCAACAGCAGCCAC--TCAGCCTGGACCTGGGAGGCGCTTCTTTTCTCAGGGACC 1965
QY 101 IleIleThrThrIleGlyThrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPhe 120
Db 1966 ATCATCACCACCATCGGCTATGGCAATGTGGCCCTGCGCACAGATGCCGGGCGCCTCTTC 2025
QY 121 CysIlePheThrAlaLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGly 140
Db 2026 TGCATCTTTTATCGCTGGTGGGGATTCGCTGTTTGGGATCTACTTGGCAGGGGTGGG 2085
QY 141 AspArgLeuGlySerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuLys 160
Db 2086 GACCGGCTGGGCTCCTCCCTCGGCCATGGCATCGGTACATTGAAGCCATCTTCTTTGAAG 2145
QY 161 TrpHisValProProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuIleGly 180
Db 2146 TGGCAGGTGCCACCGGAGCTAGTAAGAGTGTCTCGGCGATGCTTTTCTGTGATCGGC 2205
QY 181 CysLeuLeuPheValLeuThrProThrPheValPheSerTrpMetGluSerTrpSerLys 200
Db 2206 TGCCTGCTCTTTGTCTCAGCCCAAGTTCGTTCTGTCTATATGAGGACTGGAGCAAG 2265
QY 201 LeuGluAlaIleThrPheValIleValThrLeuThrThrValGlyPheGlyAspTrpVal 220
Db 2266 CTGGAGGCCATCTACTTGTATAGTACGCTTACCACCGTGGGCTTTGGCGACTATGTG 2325
QY 221 ProGlyAspGlyThrGlyGlnAsnSerProAlaTrpGlnProLeuValTrpPheTrpIle 240
Db 2326 GCCGGCGCGGACCCAGGAGGACTCCCGGCGCTATCAGCGCTGGTGTGGTTCTGGATC 2385
QY 241 LeuPheGlyLeuAlaTrpPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAla 260
Db 2386 CTGCTCGGCTGGCTTACTTCGGCTCAGTGTCTCACCACCATCGGAACTGGCTCGGAGTA 2445
QY 261 ValSerArgArgThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaAlaSerTrpThr 280
Db 2446 GTCTCCGCGGCACTCGGGCAGAGATGGCGGCGCTCAGCGCTCAGGCTGCCAGCTGGACT 2505
QY 281 GlyThrValThrAlaArgValThrGlnArgThrGlyProSerAlaProProGluLys 300
Db 2506 GGCACAGTGACAGCGGCGGTGACCCAGCGGCGGCGCGCGCGCGCGCGCGCGGAGAG 2565
QY 301 GluGlnProLeuProSerSerLeuProAlaProAlaValValGluProAlaGly 320
Db 2566 GAGCAGCCACTG-----CTGCCCTCCACCGCCCTGTCCAGCGCAGCGCGCTGGGC 2613
QY 321 ArgProGlySerProAlaProAlaGluLysValGluThrProSerProThrAlaSer 340
Db 2614 AGGCCCCGATCCCTTCGCCCCCGGAGAGGCTCAGCGGCTTCCCGCCACGCGCTCG 2673
QY 341 AlaLeuAspTrpProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSer 360
Db 2674 GCCCTGGATTATCCACGAGAACCTGGCCCTTCATCGACGAGTCTCTCGGATACGACAGC 2733
QY 361 GluArgGlyCysAlaLeuProArgAlaProArgGlyArgArgArgProAsnProSerLys 380
Db 2734 GAGCGGCGCTGCCCGCTGCCCGCGCGCGCGCGGAGAGTCCCGCGCCCAATCCCCCAGG 2793
QY 381 LysProSerArgProArgGlyProGlyArgLeuAspLysAlaValPro 397
Db 2794 AAGCCCGTGGCGCGCGCGCGCGCGCGCGCTCCCGAGACAAAGCGGTGCG 2844
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 21:56:31 ; Search time 4055.14 Seconds

(without alignments)  
3576.449 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079

Sequence: 1 MKSTYLLALLLVLLVLSG.....SKKPSRPRGRLDKAVPV 398

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USGTO	Delop 6.0	Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09655272 @CGN 1 1 4385 @runat 02022005\_141715\_6758 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.\*

1:	gb_est1.*
2:	gb_est2.*
3:	gb_hic.*
4:	gb_est3.*
5:	gb_est4.*
6:	gb_est5.*
7:	gb_est6.*
8:	gb_gsei.*
9:	gb_gsei2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	100.0	1197	9	AY405806 Mus muscu
2	1692.5	81.4	1182	9	AY405804 Homo sapi
3	1381	66.4	1560	3	CR603880 full-leng
4	1187	57.1	1405	3	BC067791 Homo sapi
5	986	47.4	581	6	CB606856 AMGNNUC:N
6	907	43.6	590	2	BE981482
7	898	43.2	736	5	EX451513
8	822.5	39.6	922	4	BI758226

10	802	38.6	2534	3	AK082153	AK082153 Mus muscu
11	788	37.9	1745	3	AK036066	AK036066 Mus muscu
12	785	37.8	2628	3	AK031904	AK031904 Mus muscu
13	784	37.7	1113	9	AY418067	AY418067 Mus muscu
14	778	37.4	1113	9	AY418065	AY418065 Homo sapi
15	760	36.6	469	2	BF565047	BF565047 UI-R-B01-
16	717.5	34.5	891	1	AL537214	AL537214 AL537214
17	684	31.9	570	2	BB569111	BB569111 BB569111
18	656.5	31.6	822	7	CK653558	CK653558 AGENCOURT
19	618.5	29.7	1113	9	AY418066	AY418066 Pan trogl
20	618	29.7	802	1	AL537215	AL537215 AL537215
21	557.5	26.8	654	7	CK005597	CK005597 AGENCOURT
22	536	25.8	920	5	BQ948206	BQ948206 AGENCOURT
23	523.5	25.2	667	5	BU759620	BU759620 UI-R-PF0-
24	510.5	24.6	537	5	EX478651	EX478651 DKF2P686H
25	494	23.8	627	7	CO039400	CO039400 UI-M-BH0-
26	491.5	23.6	879	9	AY404471	AY404471 Mus muscu
27	491	23.6	772	6	CB959623	CB959623 AGENCOURT
28	490	23.6	885	9	AY404469	AY404469 Homo sapi
29	486	23.4	553	5	BM942654	BM942654 UI-M-CG0P
30	484	23.3	498	5	BY248534	BY248534 BY248534
31	481.5	23.2	406	6	CB808226	CB808226 AMGNNUC:S
32	461.5	22.2	713	6	CB526721	CB526721 UI-M-PY0-
33	456.5	22.0	609	1	AU177116	AU177116 AU177116
34	447.5	21.5	479	6	CA871490	CA871490 K0910F08-
35	442.5	21.3	805	7	CK870719	CK870719 AGENCOURT
36	432.5	20.8	845	6	CD326083	CD326083 AGENCOURT
37	428.5	20.6	1491	3	CR622971	CR622971 full-leng
38	428.5	20.6	1493	3	CR626629	CR626629 full-leng
39	423.5	20.4	1129	4	BM544559	BM544559 AGENCOURT
40	421	20.3	3365	3	AK085330	AK085330 Mus muscu
41	416.5	20.0	775	7	CN528767	CN528767 UI-M-HQ0-
42	415.5	20.0	1360	3	AK019376	AK019376 Mus muscu
43	413.5	19.9	613	9	AY405805	AY405805 Pan trogl
44	413	19.9	801	5	BU304218	BU304218 603608750
45	412.5	19.8	4016	3	AK036882	AK036882 Mus muscu

#### ALIGNMENTS

AY405806	1197 bp	DNA	linear	GSS 15-DEC-2003
Mus musculus K09K4 gene, VIRTUAL TRANSCRIPT, partial sequence,				
genomic survey sequence.				
AY405806				
AY405806.1	GI:39761780			
GSS.				
Mus musculus (house mouse)				
Mus musculus				
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
1 (bases 1 to 1197)				
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,				
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,				
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,				
Adams, M.D. and Cargill, M.				
Inferring nonneutral evolution from human-chimp-mouse orthologous				
gene trios				
Science 302 (5652), 1960-1963 (2003)				
14671302				
2 (bases 1 to 1197)				
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,				
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,				
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,				
Adams, M.D. and Cargill, M.				
Direct Submission				
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,				
Rockville, MD 20850, USA				
This sequence was made by sequencing genomic exons and ordering				
them based on alignment				
Location/Qualifiers				
1. 1197				





[illegible]

Db	1265	GC3GCCCCGCGCGCGCGCTCCCGGACACAAAGCGGTGCGCGTG	1310
RESULT 4			
BC067791			
LOCUS		1405 bp mRNA linear HTC 26-MAR-2004	
DEFINITION		Homo sapiens cDNA clone IMAGE:30345701, with apparent retained intron.	
ACCESSION	BC067791		
VERSION	BC067791.1	GI:45768264	
KEYWORDS	HTC		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1	(bases 1 to 1405)	
AUTHORS	Strausberg, R.D., Collins, F.S., Wagner, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903 (2002)	
PUBMED	12477932		
REFERENCE	2	(bases 1 to 1405)	
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs@mail.nih.gov">cgabs@mail.nih.gov</a> Tissue Procurement: Dr. Stefan Hansson cDNA Library Preparation: Michael Brownstein / Ted Usdin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		
FEATURES			
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	1. 1405		
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	/clone="IMAGE:30345701"		
	/tissue_type="Placenta, normal"		
	/clone_lib="NIH_MGC_147"		
	/lab_host="DH10B"		
	Location/Qualifiers		
	This clone has the following problem: retained intron.		
	passed the following selection criteria: matched mRNA gi: 15718766		
	This clone was selected for full length sequencing because it		
	Series: IRAC Plate: 168 Row: 0 Column: 5		
	through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a>		
	Clone distribution: MGC clone distribution information can be found		

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/note="Vector: pBluescript"
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## ORIGIN

**Alignment Scores:**

Pred. No.:	8.2e-80	Length:	1405
Score:	1187.00	Matches:	236
Percent Similarity:	75.45%	Conservative:	16
Best Local Similarity:	70.66%	Mismatches:	28
Query Match:	75.09%	Indels:	55
DB:	3	Gaps:	3

US-09-655-272-2 (1-398) x BC067791 (1-1405)

65	LeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThrAnSerSerAsn	84	QY
246	GTGGCTGATGCCCTGGAGGGGGTGGCCAGCAAAACAACACGACCAACACAGCAGC	305	DB
85	HisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIleLeuThr	104	QY
306	CAC---TCAGCTGGACCTGGCAGCGCCTCTTTCTCAGGACCATCATCACCACC	362	DB
105	IleGlyTyrGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCysIlePheTyr	124	QY
363	ATCGGCTATGGCAATGTGGCCCTCGGCACAGATCGCGGCGCCTCTTCGCATCTTTAT	422	DB
125	AlaLeuValGlyIleProLeuPheGlyMetLeuAlaGlyValGlyAspArgLeuGly	144	QY
423	GGCGTGTGGGATTCGCGTGTGGGATCTCTACTGGCAGGGTCTGGGGACCGGCTGGGC	482	DB
145	SerSerLeuArgArgGlyIleGlyHisIleGluAlaIlePheLeuTyrHisValPro	164	QY
483	TCCTCCCTGGCCATGGCATCGGTACATTTGAAGCCATCTCTT	526	DB
165	ProGlyLeuValArgSerLeuSerAlaValLeuPheLeuIleGlyCysLeuLeuPhe	184	QY
526	-----	526	DB
185	ValLeuThrProThrPheValPheSerTyrMetGluSerTrpSerLysLeuGluAlaIle	204	QY
526	-----	526	DB
205	TyrPheValIleValThrLeuThrThrValGlyPheGlyAspTyrValProGlyAspGly	224	QY
527	-----GTACGCGTTACACACCGTGGGCTTTGGCGACTATGTGGCGCGCGGAC	574	DB
225	ThrGlyGlnAsnSerProAlaTyrGlnProLeuValTrpPheTrpIleLeuPheGlyLeu	244	QY
575	CCGAGCAGGACTCCCGGCGCTATCAGCGGTGTGTGGTCTGGATCTGTCTGGGCTG	634	DB
245	AlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArgAlaValSerArgArg	264	QY
635	GCTTACTTCGCTCAGTGTCTACACACCATCGGGAACCTGGCTGCAGTAGTGTCCCGCGC	694	DB
265	ThrArgAlaGluMetGlyGlyLeuThrAlaGlnAlaIleSerTrpThrGlyThrValThr	284	QY
695	ACTCGGCGACAGATGGCGGCGCTCAGCGCTCAGCGTCCAGCTGGAATGCGACAGTGACA	754	DB
285	AlaArgValThrGlnArgThrGlyProSerAlaProProGluLysGluGlnProLeu	304	QY
755	GC GCGGTGACCCAGCAGCGCGGCGCGCGCGCGCGCGGAGAGGAGCAGCCACTG	814	DB
305	LeuProSerSerLeuProAlaProProAlaValValGluProAlaGlyArgProGlySer	324	QY
815	-----CTGCGTCCACCGCGCTGTCCAGCGCAGCGCGTGGGCGGCGCCGATCC	862	DB
325	ProAlaProAlaGluLysValGluThrProSerProProThrAlaSerAlaLeuAspTyr	344	QY
863	CTTTGGCCCCCGAAGAGGCTCAGCGCGCTTCCCGGCCACGGCTCTGGCCCTGGATTAT	922	DB
345	ProSerGluAsnLeuAlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCys	364	QY
923	CCGAGCGAGAACCTGGCTTTCATGACGAGTCTCGGATACGACGAGCGCGGCTGC	982	DB

Qy	365	AlaLeuProAArgAlaProAArgGlyArgAArgAArgProAAsnProSerIysLysProSerAArg	394
Db	983	CCGCTGCCCGCGCGGAGAGGTGCGCGCGCCCAAAATCCCCCAGGAAGCCCGTCCGCG	1042
Qy	385	ProAArgGlyProGlyArgLeuAArgAspLysAlaValProVal	398
Db	1043	CCCCGGGCCCCGGGGGTCCCCGAGACAAAGGCGTCCCGGTG	1084
RESULT 5			
LOCUS	CB606856		
DEFINITION	AMENNUC.NRHY4-00145-Cl-A W Rat hypothalamus (10464) Rattus	linear	EST 16-MAY-2003
ACCESSION	CB606856		
VERSION	CB606856.1	GI:29546469	
KEYWORDS	EST.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (bases 1 to 581)		
AUTHORS	Angen EST Program.		
TITLE	Angen Rat EST Program		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Dan Fitzpatrick Angen, Inc One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881 Plate: 00145 row: C column: 1. Location/Qualifiers 1. 581 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /clone="nrhy4-00145-cl" /clone_lib="W Rat hypothalamus (10464)" /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat hypothalamus adult female Wistar rat avg. insert size 2.3 kb fraction 6 and 7"		
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:	4,72e-65	Length:	581
Score:	986.00	Matches:	186
Percent Similarity:	97.41%	Conservative:	2
Best Local Similarity:	96.37%	Mismatches:	5
Query Match:	47.43%	Indels:	0
DB:	6	Gaps:	0
US-09-655-272-2 (1-398) x CB606856 (1-581)			
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Db	3	ATCAAGCTGTGGCTGAAGCCCTGGGAGGGGGCGCAACCCAGAACCAAGTTGGACCAAT	62
Qy	82	SerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThrIle	101
Db	63	AGCAGCACCACTCATCAGCTTGGACCTGGGAGCGCCTTCTTTTCTCGGGGACCATC	122
Qy	102	IleThrThrIleGlyTrpGlyAsnIleValLeuHisThrAspAlaGlyArgLeuPheCys	121
Db	123	ATCACTACCATCGCTACGCAATATAGCCTTACACACAGATCGTGGGCGTCTCTTTGT	182
Qy	122	IlePheTyraLeuValGlyIleProLeuPheGlyMetLeuLeuAlaGlyValGlyAsp	141
Db	183	ATCTTCTATGCACTGTGGGGATCCCACTTTCGGGATGCTGCTGGAGTCGGGGAC	242
Qy	142	ArgLeuGlySerSerLeuAArgGlyIleGlyHisIleGluAlaIlePheLeuLysTrp	161
Db	243	CGGCTGGGCTCTCTCTGGCGCGGGGCGTCCGTCATCGACGAGTTTCTTTGAAGTGG	302
Qy	162	HisValProGlyLeuValAArgSerLeuSerAlaValLeuPheLeuLeuIleGlyCys	181

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 736)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 22, 2003 this sequence version replaced gi:31026267. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : <a href="http://www.genoscope.cns.fr">www.genoscope.cns.fr</a> 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer end enriched, double-strand cDNA was digested with Not I and cloned

into the Not 1 and EcorV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
This sequence belongs to this cluster, see  
For more information about this cluster, see  
[http://www.genoscope.cns.fr/cdna?8=CSOBAF015ZF10\\_AF01423\\_1&c=6303.f](http://www.genoscope.cns.fr/cdna?8=CSOBAF015ZF10_AF01423_1&c=6303.f)

# FEATURES

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Location/Qualifiers  
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcorV sites of the pCMVSPORT 6 vector. Library was not normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 3,14e-58 Length: 736  
Score: 898.00 Matches: 174  
Percent Similarity: 86.12% Conservative: 6  
Best Local Similarity: 83.25% Mismatches: 25  
Query Match: 43.19% Indels: 5  
DB: 5 Gaps: 1

US-09-655-272-2 (1-398) x BX451513 (1-736)

QY 190 pheValPheSerTyrMetGluSerTTPSerLysLeuGluAlaIleTyrPheValIleVal 209  
DB 9 TTCGGTTCGTG-CTTAGGAGGACTGGACAGCTGGAGGCCATCTACTTTGTTCATAGTG 67  
QY 210 ThrLeuThrThrValGlyPheGlyAspTyrValProGlyAspGlyThrGlyGlnAenSer 229  
DB 68 ACGCTTACCACCGTGGCTTGGCGATGTGTGGCGCGCGCGAGCCAGGAGGACTCC 127  
QY 230 ProAlaTyrGlnProLeuValTTPheTTPLeLeuPheGlyLeuAlaTyrPheAlaSer 249  
DB 128 CCGGCTATCAGCGCTGTGTGTGTCTGGATCTCTCGCTGCTTACTTCGCCTCA 187  
QY 250 ValLeuThrThrIleGlyAsnTTPLeuArgAlaValSerArgArgThrArgAlaGluMet 269  
DB 188 GTGCTCACCATTCGGAACTGGCTGGAGTAGTGTCCGCGCACTCGGCAGAGATG 247  
QY 270 GlyGlyLeuThrAlaGlnAlaAlaSerTTPThrGlyThrValThrAlaArgValThrGln 289  
DB 248 GCGGCTCAGCGCTCAGGCTCGAGCTGGACTGGACAGTGCAGCGCGGTGACCCAG 307  
QY 290 ArgThrGlyProSerAlaProProGluLysGluGlnProLeuLeuProSerSerLeu 309  
DB 308 CGAGCGGGCGCGCGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 355  
QY 310 ProAlaProAlaValValGluProAlaGlyArgProGlySerProAlaProAlaGlu 329  
DB 356 CTTCCACCGCCCTGTCCAGCGAGCGCTGGGCGAGCGCCCGATCCCTTCGCCCCCGAG 415  
QY 330 LysValGluThrProSerProProThrAlaSerAlaLeuAspTyrProSerGluAenLeu 349  
DB 416 AAGGCTCAGCGCTTCCCGCGCCAGCGCTCGGCTCGGATTCATCCAGCAGAGACCTG 475  
QY 350 AlaPheIleAspGluSerSerAspThrGlnSerGluArgGlyCysAlaLeuProArgAla 369  
DB 476 GCCTTCATCGACGAGTCTCGATACGACAGCGAGCGGCGGTGCGCGCGCGCGCG 535  
QY 370 ProArgGlyArgArgArgProAenProSerLysLysProSerArgProArgGlyProGly 389  
DB 536 CCAGAGGGTTCG 595

QY 390 ArgLeuArgAspLysAlaValProVal 398  
DB 596 CGTCCCCGAGACAAAGCGGTGCCGTG 622

## RESULT 8

LOCUS BE981393/c  
DEFINITION UI-M-CG0p-bdb-f-11-0-UI-s1 NIH\_BMAP\_Ret4\_S2 Mus musculus cDNA clone  
ACCESSION BE981393  
VERSION BE981393.1 GI:10650455  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 593)  
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
JOURNAL discovery  
MEDLINE Genome Res. 6 (9), 791-806 (1996)  
PUBMED 97044477

COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: MEST@mail.nih.gov

Oligo-dT track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
clones from RESEARCH GENETICS. It should be noted that Bento Soares  
is generating a small number of additional specialized  
non-redundant arrays of BMAP cDNAs whose availability will be  
considered under appropriate and limited collaborative arrangements  
The tissue for this library was contributed by Dr. Xin-Yuan Fu,  
Yale University School of Medicine  
Seq primer: M13 Forward  
POLYA=No.

## FEATURES

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Location/Qualifiers  
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polylinker; Site 1: Not I; Site 2: Eco RI; The  
NIH\_BMAP\_Ret4\_S2 library is a subtracted library.  
ultimately derived from mouse retina tissue libraries at  
various stages of development. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at [brainest.eng.uiowa.edu](http://brainest.eng.uiowa.edu). The tissue  
for this library was contributed by Dr. Xin-Yuan Fu, Yale  
University School of Medicine  
TAG\_SEQ=None found"

## ORIGIN

Alignment Scores:  
Pred. No.: 4.74e-58 Length: 593  
Score: 894.00 Matches: 176  
Percent Similarity: 99.44% Conservative: 0  
Best Local Similarity: 99.44% Mismatches: 0  
Query Match: 43.00% Indels: 1  
DB: 2 Gaps: 0

US-09-655-272-2 (1-398) x BE981393 (1-593)

QY 1 MetArgSerThrThrLeuLeuAlaLeuValLeuLeuTyrLeuValSerGly 20

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert for range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores: 2,31e-52 Length: 922  
Pred. No.: 822.50 Matches: 199  
Score: 822.50 Conservatives: 19  
Percent Similarity: 68.55% Mismatches: 39  
Best Local Similarity: 62.58% Indels: 62  
Query Match: 39.56% Gaps: 5  
DB: 4

US-09-655-272-2 (1-398) x B1758226 (1-922)

1 MetArgSerThrThrLeuLeuAlaLeuLeuValLeuLeuValSerG1 20  
134 ATGGCAGCACCACCTGCTCGGCGCTGGTCTTGTCTTACTTGTGTCTGG 193  
20 yAlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAs 40  
194 TGCCTCGTGTTCGGGCGCTGGAGCAGCCCGCAGCAGCAGCAGGAGCTGG 253  
40 pHisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAs 60  
254 GGAGGTCGAGAGAAGTTCCTGAGGGCCCATCGCTGTGTGAGCGACGAGGCTGGCCCT 313  
60 pPheLeuLysLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpTh 80  
314 CCTCATCAAGGAGGTGGTGGTGGGAGGGGTGGGAGCCGACCAACCAACGAC 373  
80 rAsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyTh 100  
374 CAGCAACAGCAGCCAC---TCAGCTGGGACCTGGCAGCGGCTCTCTTTCTCAGGGAC 430  
100 rLeuLeuThrThrLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
431 CATCATCACCACCATCGGCTATGGCATGGCCCTGGCCATGCTGGCAGGAGCTCTT 490  
120 eCysLeuPheTyAlaLeuValGlyGlyLeuProLeuPheGlyMetLeuLeuAlaGlyValG1 140  
491 CTGCAATCTTTATGCGCTGGTGGGATTCGCTGTTGGGATCTCTACTGGCAGGGCTCG 550  
140 yAspArgLeuGlySerSerLeuArgArgGlyGlyGlyHisLeuAlaLeuPheLeuLys 160  
551 GGACCGGCTGGGCTCTCTCTGCGCATGGCATGGTCCATTTGAGCCATCTTCTT--- 607  
160 sTrpHisValProGlyLeuValArgSerLeuSerAlaValLeuPheLeuLeuG1 180  
607 -----  
180 yCysLeuLeuPheValLeuThrProThrPheValPheSerTyMetGluSerTrpSerLys 200  
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200 sLeuGluAlaLeuTyPheValLeuValThrLeuThrThrValGlyPheGlyAspTyVa 220  
608 -----GTGACGCTTACCACCGTGGCTTTGGCGAGCTATGT 642  
220 lProGlyAspGlyThrGlyGlnAsnSerProAlaTyGlnProLeuValTrpPheTrp1l 240  
643 GCGCGGCGGACCCCGCAGGAGCTCCCGCGGCTATCAGCGCGCTGGTGTGGTCTGGAT 702  
240 eLeuPheGlyLeuAlaTyPheAlaSerValLeuThrThrThrThrThrThrThrThrThr 259  
703 CTTGCTCGGCGCTGGCTTACTTCCCTCAGTGTCTACCAACCAATCGGAGACTGGCTGCGA 762  
260 Ala-ValSerArgArgThrArgAla-GluMet-GlyGlyLeuThrAlaGlnAla---Ala 277  
763 GTAGGTGCGCGCGCACTCGGCGCAGAGATGGGGCGCGCTCACGGCTTCAGGGCTGCCA 822

554 ATGGCAGCACCACACTCTGCTCTGCTGGCAGCTGGTCTTACTTGTGTCTGGG 495  
21 AlaLeuValPheGlnAlaLeuGlnProHisGluGlnGlnAlaGlnLysMetAsp 40  
494 GCTCTAGTCTTCAGGCTTCGAGCAGCCTCAGAGCAGCAGGCTCAGAGAAATGGAT 435  
41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
434 CATGGCGCAGACCACTTCCTGAGGACCATCTCTGTGTGAGCCAGAGAGCTGGAGAT 375  
61 PheLeuLysLeuLeuValGluAlaLeuGlyGlyGlyAlaAsnProGluThrSerTrpThr 80  
374 TTCATCAGCTCTCTGTTGAAGCCCTGGGAGGGCGCAACCCAGAAACACAGCTGGACC 315  
81 AsnSerSerAsnHisSerSerAlaTrpAsnLeuGlySerAlaPhePheSerGlyThr 100  
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101 lLeuLeuThrThrLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
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121 CysLeuPheTyAlaLeuValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 140  
194 TGTATCTTATGACACTGGTGGGATCCCACTGTTCGGGATGCTGCTGGCGGAGTCTGGG 135  
141 AspArgLeuGlySerSerLeuArgArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160  
134 GACCGGCTGGGCTCTCTCTGCGCGCGGGGATCGGCACATCGCAGCAATCTCTTGAAG 75  
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RESULT 9  
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DEFINITION mRNA sequence.  
ACCESSION B1758226  
VERSION B1758226.1 GI:15749804  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue procurement: Life Technologies, Inc.  
cDNA Library Prepared by: The I.M.A.G.E. Consortium (ILNL)  
cDNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
plate: LLAM1501 row: m column: 18  
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Site 2: EcoRV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is oligo-dT

FEATURES  
source

Qy 278 SerTrpThr---GlyThrValThrAlaArg-ValThrGlnArgThrGlyPro---SerAl 295  
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 Qy 295 aProProGlu-LysGluGlnProLeuLeuProSer 307  
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 Db 883 CCGGCGCGCGCACGAAGGACGACACTGGTGTGCTTCA 920  
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RESULT 10  
 LOCUS AK082153  
 DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length  
 enriched library, clone:C230015H11 product:POTASSIUM CHANNEL  
 SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL  
 TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog [Rattus norvegicus],  
 full insert sequence.

ACCESSION AK082153  
 VERSION AK082153.1 GI:26349568  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kifunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

URL:http://genome.gsc.riken.jp/  
 URL:http://fantom.gsc.riken.jp/  
 URL:http://Location/Qualifiers

## FEATURES

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## ORIGIN

Alignment Scores:  
 Pred. No.: 3-22e-50 Length: 2534  
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 Percent Similarity: 59.90% Conservative: 68  
 Best Local Similarity: 43.68% Mismatches: 129  
 Query Match: 38.58% Indels: 41  
 DB: 3 Gaps: 11

US-09-655-272-2 (1-398) x AK082153 (1-2534)

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 Qy 41 HisGlyArgAspGlnPheLeuArgAspHisProCysValSerGlnLysSerLeuGluAsp 60  
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QY 61 PheileLysLeuLeuValGluAlaLeuGlyGlyAlaAsnProGluThrSerTrpThr 80  
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 QY 221 ProGlyAspGlyThrGlyGlnAsn---SerProAlaTyrGlnProLeuValTrpPheTrp 239  
 Db 954 GCAGGGGAAATGCTGGCATCAATTTACCGAGGTTGACAGCGCGTGGTGGTTTGG 1013  
 QY 240 IleLeuPheGlyLeuAlaTyrPheAlaSerValLeuThrThrIleGlyAsnTrpLeuArg 259  
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 QY 291 -----ThrGlyProSerAlaProProProGlu----- 299  
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 Db 1369 ACCTAGCCCTTAAGGGGCGCAGAACAGCTTACCAACATGGGCGGCGCTTCTGAGGACA 1428  
 QY 355 SerSerAspThrGlnSerGluArgGlyCysAlaLeuProArgAlaProArgGlyArg--- 373  
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 QY 374 -----ArgArgProAsnProSer-----LysLysProSerArgProArgGly 387  
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AK036066 1745 bp mRNA linear HTC 03-APR-2004  
 LOCUS Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length  
 DEFINITION enriched library, clone:9630032C21 product:POTASSIUM CHANNEL  
 SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN  
 TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog (Rattus norvegicus),  
 full insert sequence.  
 AK036066  
 ACCESSION AK036066.1 GI:26331129  
 VERSION AK036066.1  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
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 sequencing pipeline with 384 multipillarary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
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 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 1745)  
 JOURNAL Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayaashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
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 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)





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 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636  
 2  
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 11042159  
 3  
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 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
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 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
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 Genome Res. 10 (11), 1757-1771 (2000)  
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 FANTOM Consortium.  
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 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
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 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 2628)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T.,  
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 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216  
 CDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
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DEFINITION Mus musculus Kcnk2 gene, VIRTUAL TRANSCRIPT, partial sequence,
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VERSION 1
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1113)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBLISHED 14671302
AUTHORS 2 (bases 1 to 1113)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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US-09-655-272-2 (1-398) x AY418067 (1-1113)

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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1113)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
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Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
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AUTHORS Bonaldo,M.F., Lemmon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548

## COMMENT

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID= 1798469  
 Seq primer: M13 Forward.

## FEATURES

Location/Qualifiers

source

1. .469

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 corpus striatum and hippocampus. For a detailed  
 description of the library from which this clone was  
 derived, please visit our web site at  
 ratseq.eng.uiowa.edu. The subtraction has been previously  
 described in (Bonaldo, Lennon and Soares, Genome Research  
 6:791-806, 1996)"

## ORIGIN

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US-09-655-272-2 (1-398) x BF565047 (1-469)

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ORIGIN

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Qy	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle	80
Db	664	GGAGCGCGGTGTTCAAGGCATTGGAGCAGCTCAGAGATTTCCTCCAGAGACCACT	723
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
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Qy	101	GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
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Qy	121	SerAsnGlnValSerHisTlPAspLeuGlySerSerPhePheAlaGlyThrValIle	140
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Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160
Db	904	ACACCATAGGATTTGGAAACATCTCCCAACGAACTGAAGTGGAAAAATATTTCTGCATC	963
Qy	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln	180
Db	964	ATCATGCTCTGGGAAATTCCTCTTGTGCTTCTACTGCTGGGTTGGTGTATCAG	1023
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Qy	201	ValSerGlnThrLysIleArgIleSerThrIlePheIleLeuPheGlyCysVal	220
Db	1084	GTTAGTCAGACGAAGATTCGTATCATCTCCACATCATCTTCTGCTGCTGGCTGTC	1143
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
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Qy	241	AlaIleTyrPheValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly	260
Db	1204	GCTATCTATTGTTGGTATCACTCTGACGACCATTTGGATTGGAGACTACGTGGAGGT	1263
Qy	261	GlySerAspIleGluTyrLeuAspPheTyrLysProValValTlPThrIleLeuVal	280

Db	1264	GGATCAGACATTGAATATCTGAGCTTCTACAAGCCCTGTGCTGTGGTCTCGATT	1323
Qy	281	GlyLeuAlaTyrPheAlaValLeuSerMetIleGlyAspTlPLeuArgValIleSer	300
Db	1324	GGGCTGCGCTTACTTTGAGCATGTTCTGAGCATGATTGGGAGCTGCTACGGGTATCTCT	1383
Qy	301	LysLysThrLysGluValGluValGlyGluPheArgAlaHisAlaAlaGluTlPThrAlaAsn	320
Db	1384	AAGAAGACGAGAGAGAGGTGGGAGATTTCAGAGCGCATGCGCTGAGTGGACGCAAT	1443
Qy	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTlPAspLysPhe	340
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Qy	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln	360
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RESULT 2			
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LOCUS			
DEFINITION			
Novel mammalian potassium channel families having mechanical			
sensitivity activated by polyunsaturated fatty acid, and method for			
using them particularly for drug screening.			
ACCESSION			
BD140671			
VERSION			
BD140671.1 GI:23235616			
KEYWORDS			
JP 2002505102-A/2.			
SOURCE			
unidentified			
ORGANISM			
unclassified.			
REFERENCE			
1 (bases 1 to 1993)			
Honore,E., Fink,M., Lazdunski,M., Lesage,F. and Duprat,F.			
Novel mammalian potassium channel families having mechanical			
sensitivity activated by polyunsaturated fatty acid, and method for			
using them particularly for drug screening			
Patent: JP 2002505102-A 2 19-FEB-2002;			
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE			
JOURNAL			
OS Unidentified			
COMMENT			
PN JP 2002505102-A/2			
PD 19-FEB-2002			
PF 23-FEB-1999 JP 2000534640			
PR 05-MAR-1998 FR 98/02725			
PI ERIC HONORE,MICHEL FINK,MICHEL LAZDUNSKI,FLORIAN LESAGE, PI			
FABRICE DUPRAT			
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PC C12N1/15,			
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02,G01N33/			
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Strandedness: Double;			
CC Topology: Linear;			
CC Novel mammalian potassium channel families having mechanical			
sensitivity			
activated by polyunsaturated fatty acid, and method for using			
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CC particularly for drug screening			
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FEATURES  
source

ORIGIN



## Alignment Scores:

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Score: 1893.00 Matches: 370  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

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QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
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ACCESSION AR156460  
VERSION AR156460.1 GI:15125164  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1994)  
AUTHORS Meadows H.Jane. and Chapman, C.Gerald.  
TITLE h-TREK1 polypeptides and h-TREK1 polynucleotides  
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SEQUENCE 5 from Patent WO9937762.
ACCESSION AX003051
VERSION AX003051.1 GI:9926936
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Chapman, C.G. and Meadows, H.J.
AUTHORS Trek-1 like two pore potassium channel
TITLE Patent: WO 9937762-A 5 29-JUL-1999;
JOURNAL SMITHKLINE BEECHAM PLC (GB)
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Query Match: 99.31% Indels: 0
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Qy 201 ValSerGlnThrLysIleArgIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1084 GTTAGTCACAGCAAGATTCGTATCATCTCCACCATCATCTTCATCTCTTGTGGCTGTGC 1143
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Db 1564 GAACTGACTCCGTGTATGAGGACC 1587

RESULT 6
BD273739 3580 bp DNA linear PAT 17-JUL-2003
LOCUS Method for identifying anesthetic drug.
DEFINITION BD273739
ACCESSION BD273739
VERSION BD273739.1 GI:33083507
KEYWORDS JP 2002536017-A/2.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 3580)
Lazdunski, M., Honore, E., Lesage, F., Roney, G. and Patel, A.J.
Method for identifying anesthetic drug
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JOURNAL Patent: JP 2002536017-A 2 29-OCT-2002;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS)  
COMMENT OS Mus musculus (mouse)  
PD JP 2002536017-A/2  
PD 29-OCT-2002  
PF 11-FEB-2000 JP 2000598636  
PR 12-FEB-1999 US 60/119727,11-FEB-2000 US 09/503089 PI  
MICHEL LAZDUNSKI, ERIC HONORE, FLORIAN LESAGE, GEORGES ROMÉY, FI  
AMANDA J PATEL  
PC C12N15/09, C07K14/47, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50// PC  
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U73488  
VERSION U73488.2 GI:4584798  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
REFERENCE 1 (bases 1 to 3580)  
AUTHORS Fink, M., Duprat, F., Lesage, F., Reyes, R., Romey, G., Heurteaux, C. and Lazdunski, M.  
TITLE Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel  
JOURNAL EMBO J. 15 (24), 6854-6862 (1996)  
MEDLINE 97157476  
PUBMED 9003761  
REFERENCE 2 (bases 1 to 3580)  
AUTHORS Fink, M., Duprat, F., Lesage, F., Reyes, R., Romey, G., Heurteaux, C. and Lazdunski, M.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-1996) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France  
REFERENCE 3 (bases 1 to 3580)  
AUTHORS Fink, M., Duprat, F., Lesage, F., Reyes, R., Romey, G., Heurteaux, C. and Lazdunski, M.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France  
REMARK Sequence update by submitter  
COMMENT On Apr 15, 1999 this sequence version replaced gi:1794281.  
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## ORIGIN

## Alignment Scores:

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 Query Match: 98.99% Indels: 0  
 DB: 10 Gaps: 0

US-09-655-272-4 (1-370) x MMU73488 (1-3580)

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## RESULT 8

## BC062094

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

BC062094 3228 bp mRNA linear ROD 06-JAN-2004  
 Mus musculus potassium channel, subfamily K, member 2, mRNA (cdna  
 clone MGC:69619 IMAGE:684897), complete cds.

BC062094

BC062094.1

GI:38566066

MGC.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3228)

Strausberg, R. U., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, P.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. B., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalón, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahy, J., Helton, E., Kettner, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smalls, D. E.,

Schurch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

human and mouse cDNA sequences

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 3228)

Strausberg, R.

Direct Submission

Submitted (13-NOV-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgi.nci.nih.gov>

Contact: MGC help desk

REMARK

COMMENT

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Email: cgabs@mail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@cgsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marza.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 132 Row: P Column: 11  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 6754431.

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this family is 6 transmembrane helices in which the last  
two helices flank a loop which determines ion selectivity.  
In some sub-families (e.g. Na channels) the domain is  
repeated four times, whereas in others (e.g. K channels)  
the protein forms as a tetramer in the membrane. A  
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two helices but is not the Pfam family due to it lacking  
the first four helices"  
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gene

CDS

misc\_feature

ORIGIN

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Best Local Similarity: 99.18% Mismatches: 2

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DEFINITION cds.
ACCESSION AF325671
VERSION AF325671.1 GI:15528824
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3187)
AUTHORS Bockenhauer, D., Zilberberg, N. and Goldstein, S.A.
TITLE KCNK2: reversible conversion of a hippocampal potassium leak into a
voltage-dependent channel
JOURNAL Nat. Neurosci. 4 (5), 486-491 (2001)
MEDLINE 21219399
PUBMED 11319556
REFERENCE 2 (bases 1 to 3187)
AUTHORS Bockenhauer, D. and Goldstein, S.A.N.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-2000) Pediatrics, Section of Developmental
Biology and Biophysics, Yale University Medical School, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA

FEATURES
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ORIGIN
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Thu Feb 3 07:31:03 2005

LOCUS AF385402 3291 bp mRNA linear ROD 07-MAY-2002  
DEFINITION Rattus norvegicus tandem pore domain potassium channel TREK-1 mRNA, complete cds.  
ACCESSION AF385402  
VERSION AF385402.1 GI:19716295  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 3291)  
AUTHORS Gu, W., Schlachet, G., Hirsch, J.R., Engels, H., Karschin, C., Karschin, A., Derst, C., Steinlein, O.K. and Daut, J.  
TITLE Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain potassium channel TREK-2  
JOURNAL J. Physiol. (Lond.) 539 (Pt 3), 657-668 (2002)  
MEDLINE 21896087  
PUBMED 11897838  
REFERENCE 2 (bases 1 to 3291)  
AUTHORS Derst, C. and Daut, J.  
TITLE Direct Submision  
JOURNAL Submitted (25-MAY-2001) Lab EEG, Inst. of Human Genetics, Wilhelmstr. 31, Bonn 53111, Germany  
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VERSION AV148474.1 GI:23630232  
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SOURCE Bos taurus  
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REFERENCE 1 (bases 1 to 1534)



AUTHORS Enyeart,J.J., Xu,L., Danthi,S. and Enyeart,J.A.  
 TITLE An ACTH- and ATP-regulated Background K<sup>+</sup> Channel in Adrenocortical  
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 J. Biol. Chem. 277 (51), 49186-49199 (2002)  
 PUBMED 12368289  
 REFERENCE 2 (bases 1 to 1534)  
 AUTHORS Enyeart,J.J. and Enyeart,J.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-SEP-2002) Neuroscience, The Ohio State University  
 College of Medicine, 5190 Graves Hall, 333 W. 10th Ave, Columbus,  
 OH 43210, USA

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 PD 29-OCT-2002  
 PF 11-FEB-2000 JP 2000598636  
 PR 12-FEB-1999 US 60/119727, 11-FEB-2000 US 09/503089 PI  
 MICHEL LAZDUNSKI, ERIC HONORE, FLORIAN LESAGE, GEORGES ROMEY, PI  
 AMANDA J PATEL

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LOCUS

DEFINITION

ACCESSION

VERSION

SOURCE

ORGANISM

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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1246)
AUTHORS Meadows,H.Jane, and Chapman,C.Gerald.
TITLE h-TREK1 polypeptides and h-TREK1 polynucleotides
JOURNAL Patent: US 6242217-A 1 05-JUN-2001;
FEATURES
Location/Qualifiers
1..1246
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Pred. No.: 5,82e-160 Length: 1246
Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservatives: 8
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 6 Gaps: 0

US-09-655-272-4 (1-370) x AR156458 (1-1246)
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QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerSerAlaIleAen 40
DB 69 TCGTTTTCACGAACCCACAGTCTTCTCCCGGTGGAGAGTGACACGACCATTAAT 128
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLeuIle 60
DB 129 GTTATGAATGGAGAGCGTCTCCAGATATCTCTGTGTCTCTCTATCTGATCATC 188
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
DB 189 GGAGCCACCGTGTTCAAAGCATTGGAGCAGCTCATGAGATTTCACAGAGACCCATT 248
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHieAlaCysValAenSerThrGluLeuAsp 100
DB 249 GTGATCCAGAAAGCAACATTCAATCCCAACATTCTCTGTGTCAATTCGACGAGCTGGAT 308
QY 101 GluLeuIleGlnIleValAlaAlaIleAenAlaGlyIleIleProLeuGlyAenSer 120
DB 309 GAATCATTCAGCAATAGTGGAGCAATAAATTCAGGGATTATACCGTTAGGAAACACC 368
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PC C12P21/02, C12Q1/68, G01N33/15, G01N33/50, C12N15/00, A61K37/02 CC  
TREK1-like two-hole potassium channel  
FH Key Location/Qualifiers  
FT source 1..1246  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source

# ORIGIN

Alignment Scores:  
Pred. No.: 5,82e-160 Length: 1246  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 6 Gaps: 0

US-09-655-272-4 (1-370) x BD228720 (1-1246)

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QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
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QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
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QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
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DB 729 GCCATTTATTTTGGTTATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 788

141 ThrThrIleGlyPheGlyAenIleSerProArgThrGluGlyGlyIlePheCysIle 160  
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QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
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QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAen 200  
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QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAenHisAenGln 360  
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LOCUS  
DEFINITION TREK1-like two-hole potassium channel.  
ACCESSION BD228720  
VERSION BD228720.1 GI:33038490  
KEYWORDS JP 2002511233-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1246)  
AUTHORS Meadows,H.J. and Chapman,C.G.  
TITLE TREK1-like two-hole potassium channel  
JOURNAL Patent: JP 2002511233-A 1 16-APR-2002;  
SMITHKLINE BEECHAM PLC  
COMMENT OS Homo sapiens (human)  
PN JP 2002511233-A/1  
PD 16-APR-2002  
PR 02-DEC-1998 JP 2000528670  
PF 27-JAN-1998 EP 98300570.3, 09-OCT-1998 GB 9822135.1 PI  
HELEN JANE MEADOWS, CONRAD GERALD CHAPMAN  
PC C12N15/09, A61K38/00, C07K14/705, C07K16/28, C12N1/15, C12N1/19, PC  
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Db |||||||
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QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe 340
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QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyValAsnHisAsnGln 360
Db |||||||
1029 CAGCGGGCCACCTTCATCAAGCGGAAGCTCTCGGCAGAACTGGCTGGAAACCAACATCAG 1088
QY 361 GluLeuThrProCysMetArgThr 368
Db |||||||
1089 GAGCTGACTCCTTGTTAGGAGACC 1112
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Job time : 5229.76 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 20:13:51 ; Search time 566.562 Seconds

(without alignments)  
3428.193 Million cell updates/sec

Title: US-09-655-272-4

Perfect score: 1883

Sequence: 1 MAAPLLDPKSAQNSKPL.....SALAGNHQELTPCMTCL 370

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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1870	99.0	1994	2 AAZ00040	Aaz00040 Mouse h-T
3	1864	99.0	3580	3 AAD17497	Aad17497 Murine TR
4	1833	97.3	1236	3 AAD17496	Aad17496 Human TRE
5	1833	97.3	1246	2 AAZ00039	Aaz00039 h-TREK1 p
6	1833	97.3	1246	4 AAC90412	Aac90412 Human TRE

7	1833	97.3	3300	2 AAZ11915	Aaz11915 Human pot
8	1827	97.0	2391	11 ADP03564	Adp03564 Human GPC
9	1805	95.9	2130	4 AAS12169	Aas12169 Human pot
10	1801	95.6	2130	4 AAS12181	Aas12181 Human pot
11	1800	95.6	2130	4 AAS12182	Aas12182 Human pot
12	1797	95.4	2130	4 AAS12184	Aas12184 Human pot
13	1796	95.4	2130	4 AAS12183	Aas12183 Human pot
14	1743.5	92.6	3393	8 ACC46425	Acc46425 Human dlt
15	1447	76.8	1702	12 ADJ27238	Adj27238 Human TRI
16	1247.5	66.3	1614	6 AAI72558	Aai72558 ORF of hu
17	1247.5	66.3	1614	6 AAD27459	Aad27459 Human TRE
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19	1247.5	66.3	1632	6 ABR27503	Abk27503 DNA encod
20	1247.5	66.3	1644	6 ABN85879	Abn85879 Hypochala
21	1247.5	66.3	1870	10 ADE07404	Ada07404 Novel cod
22	1247.5	66.3	2028	8 ADA05745	Ada05745 Human NOV
23	1247.5	66.3	2028	12 ADN62909	Adn62909 Human NOV
24	1247.5	66.3	2065	6 ABK49585	Abk49585 Human CDN
25	1247.5	66.3	2730	6 ABZ11550	Abz11550 Human pol
26	1247.5	66.3	2730	12 ADM44068	Adm44068 Novel hum
27	1220	64.8	2820	6 AAL44676	Aal44676 Human tra
28	808	42.9	779	4 AAH98807	Aah98807 Human EST
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30	797	42.3	1182	3 AAZ27105	Aaz27105 Human h-T
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32	797	42.3	1218	3 AAA27106	Aaa27106 Human h-T
33	797	42.3	1257	6 AAH99922	Aah99922 Nucleotid
34	797	42.3	1257	12 ADI27937	Adi27937 Human TWI
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36	797	42.3	1408	6 AAH99921	Aah99921 Nucleotid
37	797	42.3	1408	10 ADK52549	Adk52549 Hematolog
38	797	42.3	1408	12 ADH51638	Adh51638 Human 123
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40	797	42.3	2772	10 AAD58498	Aad58498 Human pot
41	797	42.3	2772	12 ADP21365	Adp21365 Gene KCN
42	797	42.3	3945	8 ABX91950	Abx91950 Human G p
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## ALIGNMENTS

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AC AAZ10607;  
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DT 18-NOV-1999 (first entry)  
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DE cDNA encoding a mechanically sensitive potassium channel protein TREK-1.  
XX  
KW Mechanically sensitive potassium channel protein; TREK-1;  
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease; ds.  
XX  
OS Mus sp.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 484..1596  
FT /\*tag= a

PN WO9945108-A2.

XX 10-SEP-1999.

PF 23-FEB-1999; 99WO-FR000404.

PR 05-MAR-1998; 98PR-0002725.

PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Honore E, Fink M, Lazdunski M, Leseage F, Duprat F;  
 XX WPI; 1999-551038/46.  
 DR P-PSDB; AAY30648.  
 XX New mechanically sensitive potassium channel, used to screen for specific  
 PT modulators, potential therapeutic agents for heart and nervous system  
 PT disorders.  
 XX Claim 7; Page 23-25; 40pp; French.  
 XX The present sequence encodes a mechanically sensitive potassium channel  
 CC protein designated TREK-1. The protein is activated by polyunsaturated  
 CC fatty acids, particularly arachidonic acid, and by riluzole. The protein  
 CC is used to screen for specific modulators which are useful for treating  
 CC or preventing diseases of the heart and nervous systems in humans and  
 CC animals, e.g. epilepsy, cardiovascular disease (arrhythmia),  
 CC neurodegeneration (particularly where associated with ischemia or  
 CC anoxia), abnormalities of hormone secretion and muscular disease. The  
 CC protein itself may be used to treat these diseases. Antibodies specific  
 CC for the protein are used to detect it in tissues, also as therapeutic  
 CC inhibitors or activators  
 XX Sequence 1993 BP; 426 A; 570 C; 561 G; 436 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 1.58e-213 Length: 1993  
 Score: 1883.00 Matches: 370  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaAlaAsn 40  
 DB 544 TCATCTCTTCAAAACCCACCGCTGCTTCCCGGGTGGAGAGTGACTCGGCCATTAAAT 603  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
 DB 604 GTTATGAATGGAAGACAGTCTCCACGATTTCTTGGTGGTCTCTTCTTCTTCTTCTTCT 663  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80  
 DB 664 GGAGCGCGGTGTTTCAGGCATTGGAGCAGCTCAGGAGATTTCACAGAGGACCACCAATT 723  
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 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
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 QY 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 964 AUCTATGCGCTTGTGGGAATTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1023

QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
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 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
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 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
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 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1384 AAGAAGACGAAGAGAGGTGGAGAGTTTCAGAGCGCATCCCGCTGAGTGGACAGCCCAAT 1443  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTrpAspLysPhe 340  
 DB 1444 GTACGCGCGGAGTTCAAGAAACGAGGAGCGGCTGAGCGTGGAGATCTACGACAGTTC 1503  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1504 CAGCGTGCACATCCGTGAAGCGGAAGCTCTCCGACAGCTGGCGGGGCACACACACAG 1563  
 QY 361 GluLeuThrProCysMetArgThrCysLeu 370  
 DB 1564 GAATGACTCCGTGTATGAGACCTGTCTG 1593

RESULT 2  
 AAZ00040  
 ID AAZ00040 standard; DNA; 1994 BP.  
 XX AC AAZ00040;  
 XX 12-OCT-1999 (first entry)  
 XX Mouse h-TREK1 polynucleotide.  
 XX h-TREK1; two pore potassium channel; inflammatory disease;  
 XX chromosome 1q32; ss.  
 XX Mus musculus.  
 XX Key Location/Qualifiers  
 XX CDS 484..1719  
 XX /tag= a  
 XX /product= "h-TREK1"  
 XX WO9937762-A1.  
 XX 29-JUL-1999.  
 XX 02-DEC-1998; 98WO-EF007805.  
 XX 27-JAN-1998; 98EP-00300570.  
 XX 09-OCT-1998; 98GB-00022135.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Meadows HJ, Chapman CG;  
 XX



DR WPI; 1999-469126/39;  
 XX P-PSDB; AAY28497.  
 CC New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases.  
 XX Claim 9; Page 25-26; 44pp; English.  
 PS  
 XX This sequence is the h-TREK1 polynucleotide from the mouse, encoding the  
 CC h-TREK1 polypeptide AAY28496. h-TREK1 is a two pore potassium channel.  
 CC The polynucleotide sequence of h-TREK1 can be used to diagnose a disease  
 CC or susceptibility to a disease related to expression or activity of h-  
 CC TREK1 polypeptides. The methods of diagnosis may be used in the treatment  
 CC of diseases including cancer, pulmonary, cardiovascular, and inflammatory  
 CC diseases, pain, psychiatric disorders including depression and  
 CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
 CC and head trauma and neurological disorders including migraine  
 XX  
 SQ Sequence 1994 BP; 426 A; 561 C; 561 G; 446 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5,596-212 Length: 1994  
 Score: 1870.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.31% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-655-272-4 (1-370) x AAZ00040 (1-1994)  
 QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 484 ATGGCGGCCCTGACTTGGTATCCCAAGTCTGCTCAGAACTCCAAACCGAGGCTC 543  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 DB 544 TCATCTCTTCAAAACCCACCGGTGCTGCTTCCGGGTGGAGTGAAGTCCGGCCATTAT 603  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIleIle 60  
 DB 604 GTTATGAATGGAAGACAGCTCCACGATTTTCTGTGTGTCTCTACCTGATCATC 663  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluInProGlnGluIleSerGlnArgThrIle 80  
 DB 664 GGAGCCGCGGTGTCAAGGCATTGGAGCAGCTCCAGAGATTTCACAGAGGACCACTT 723  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 724 GTATCCAGAACGACAGACCTTCATAGCCAGCATGCTGCTGCTCACTCCACCGAGCTGGAC 783  
 QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 784 GAACTCATCCAGCAATAGTGGCAGCAATAAACGAGGATTTATCCCTTAGGAACACG 843  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePhePheAlaGlyThrValIle 140  
 DB 844 TCCAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTTCTTCTGCTGCTGCTATC 903  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160  
 DB 904 ACAACATAGGATTGGAAACATCTCCACGAACTGAAGGTGGAATAATTTCTGCATC 963  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180  
 DB 964 ATCTATGCCTTGTGGGAATTCCTCTTTGGCTTCTACTGCTGGGTGTGTATCAG 1023  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 1024 CTAGGAACATATTTGGAAAGGAATTCGCAAGTGGAAACACATTTTATTAAGTGAAT 1083  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 1084 GTTAGTCAGACGAAGATTGATATCATCTCCACCATCATCTTCTGCTGTGCTGTGTC 1143

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 1144 CTCTTTGTGGCTCTCCCTGGCTCATATTCAAGCACATAGAAGCTGGAGCGCCCTGGAC 1203  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 1204 GCTATCTATTTTGTGGTTATCACTCTGACGACCATTTGGATTGGAGACTACGTGGCAGGT 1263  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 1264 GATCAGACATTGAATATCTGACCTCTACAGCCCTGTGGTGTGTTCTGGATCCTCGTT 1323  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1324 GGGCTGGCCCTACTTTCGACCTGTTCTGACATGATTTGGGACTGGCTACGGGTGATCTCT 1383  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1384 AAGAAGACGAAGAAAGAGGTGGAGATTTCAGAGCGCATGCCGCTGAGTGGACAGCCAAT 1443  
 QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValIleLysPheLysPhe 340  
 DB 1444 GTCAAGCGCGAGTTCAAGGAACAGAGGAGCGCTGAGGATCTACGACAGTTTC 1503  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1504 CAGCGTGCACATCCGTGAAGCGGAAGCTCTCCGAGAGCTGGCGGCAACCAACACAG 1563  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1564 GAACTGACTCCGTGATGAGGACC 1587  
 RESULT 3  
 AAD17497  
 ID AAD17497 standard; DNA; 3580 BP.  
 XX AAD17497;  
 DT 10-DEC-2001 (first entry)  
 XX Murine TREK-1 potassium channel protein DNA.  
 DE Murine TREK-1 potassium channel protein DNA.  
 XX Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia; ds.  
 XX Mus musculus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 484..1719  
 FT /\*tag= a  
 FT /product= "Murine TREK-1 potassium channel protein"  
 PN WO200047738-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-IB0000226.  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
 XX  
 DR WPI; 2000-549146/50.  
 DR P-PSDB; AAE10342.  
 XX  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anesthetic  
 PT properties.  
 XX

PS Claim 7; Page 29-31; 39pp; English.

XX The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present DNA sequence encodes murine TREK-1 potassium channel protein

XX Sequence 3580 BP; 870 A; 917 C; 913 G; 880 T; 0 U; 0 Other;

Alignment Scores: 7,07e-211 Length: 3580  
 Pred. No.: 1864.00 Matches: 367  
 Score: 99.73% Conservative: 0  
 Percent Similarity: 99.73% Mismatches: 1  
 Best Local Similarity: 99.73% Indels: 0  
 Query Match: 98.99% Gaps: 0  
 DB: 3

US-09-655-272-4 (1-370) x AAD17497 (1-3580)

Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 Db 484 ATGGCGGCCCTGACTTGGTGGATCCCAAGTCTGCTCGAAGCTCCAAACCGAGGCTC 543  
 Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 Db 544 TCATTCTCTCAAAACCCACCGCTGCTTCCCGGGTGGAGAGTGAATCGGCCATTAAAT 603  
 Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIle 60  
 Db 604 GTTATGAATGGAAGACAGTCTCCACGATTTCTGTTGGTGGTGCCTTCTACCTGATCA 663  
 Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
 Db 664 GGAGCGCGGTGTTCAAGSCATTGGAGCAGCTCCAGAGATTTCCAGAGACCCACCAT 723  
 Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 724 GTATCCAGACAGACACCTTCATAGCCAGCATGCTGCTGCAACTCCACGAGCTGGAC 783  
 Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 784 GAACTCATCCAGCAATAGTGCACATATAACGAGGATATCCCTTAGGAAACAGC 843  
 Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 Db 844 TCCATCAAGTTAGTCACTGGGACCTCGAAGCTCTTTCTTTTGGTGGTACTGTTATC 903  
 Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 904 ACAACCATAGGATTTGGAAACATCTCCCAAGTGAAGACACATTTATTAAGTGGAT 963  
 Qy 161 IleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 964 ATCTATGCCCTGCTGGGAATTTCCCTCTTTGGCTTTCTACTGGCTGGGGTGGTATCAG 1023  
 Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 1024 CTAGGAACATATATTGGAAAGGAATTTGCCAAGTGAAGACACATTTATTAAGTGGAT 1083  
 Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 1084 GTTAGTCAGACGAGATTCGTATCATCTCCACCATCATCTTCTCTGTTGGCTGTGTC 1143  
 Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 1144 CTCCTTTGGCTCTCCCTGGGTCATATTCAAGCATAGAAGCTGGAGCCCTGGAC 1203  
 Qy 241 AlaIleTrpPheValIleThrLeuThrIleGlyPheGlyAspTrpValAlaGly 260

Db 1204 GCTATCTATTGTTGTTATCACTCTGACGACCACTGGATTGGAGACTAGTGGCAGGT 1263  
 Qy 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal 280  
 Db 1264 GGATCAGACATTGAATATCTGGACTTCTACAGCTGTGGTGTGTTCTGGATCTCGTT 1323  
 Qy 281 GlyLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 Db 1324 GGCTGGCTCTTTCAGCTGTCTTCTGACATGATTGGGACTGGCTACGGGTGATCTCT 1383  
 Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 Db 1384 AAGAAGACGGAAGAGAGGTGGAGATTTCAGAGCCATGCCGCTGAGTGGACAGCAAT 1443  
 Qy 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTrpAspLysPhe 340  
 Db 1444 GTACGCCCGAGTTCAAGGAACAGAGAGCGGCTGAGCGTGGAGATCTACGACAAAGTTC 1503  
 Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyValAsnHisAsnGln 360  
 Db 1504 CAGCGTGCACATCCCGTGAAGCGGAAGCTCTCCGACAGCTGGCGGGCAACCAACACAG 1563  
 Qy 361 GluLeuThrProCysMetArgThr 368  
 Db 1564 GAACTGACTCCGTGTAGAGAGACC 1587  
 RESULT 4  
 AAD17496  
 ID AAD17496 standard; DNA; 1236 BP.  
 XX  
 AC AAD17496;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Human TREK-1 potassium channel protein DNA.  
 XX  
 KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia; amnesia; db.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT /tag= a  
 FT /product= "Human TREK-1 potassium channel protein"  
 XX  
 PN WO200047738-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-IB000226.  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
 FI WPI; 2000-549146/50.  
 XX  
 DR P-PSDB; AAEE10341.  
 XX  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic properties.  
 FT  
 XX Claim 1; Page 26-28; 39pp; English.  
 XX  
 CC The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe,

CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present DNA sequence encodes human TREK-  
CC 1 potassium channel protein

XX Sequence 1236 BP; 330 A; 279 C; 299 G; 328 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6, 92e-208 Length: 1236  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x AAD17496 (1-1236)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu 20  
DB 1 ATGGCGCCCTGACTTCTGGATCTCTTAATCTCCGCTCAGAACTCCAAACCGAGCTC 60  
QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAen 40  
DB 1 TCCTTTTCCACGAACCCACAGTCTTCTCCGGGTGGAGAGTGACACGACCATTAAT 120  
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuIleIle 60  
DB 121 GTTATGAAATGGAAGACGGTCTCCAGATATCTCGTGGTGTCTCTCTATCTGATCATC 180  
QY 61 GlyAlaAlaValPheLysAlaLeuGluInProGlnGluLeuSerGlnArgThrIle 80  
DB 181 GGAGCACCGTGTCAAGACATTTGGAGCAGCCCTCATGAGATTTCCAGAGGACCACTT 240  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 241 GTGATCCAGAGCAACATTCATATCCACACATCTCTGTGTCAATTCGAGGAGCTGGAT 300  
QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAenSer 120  
DB 301 GAACCTATTCAGCAATAGTGGCAGCAATAAATGACGGGATATATACCGTTAGGAACACC 360  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 361 TCCATCAATACAGTCACTGGGATTTGGGAGTTCTCTCTTCTGCTGCACTGTATT 420  
QY 141 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160  
DB 421 ACAACCATAGATTGGAAACATCTCCACGACACAGAGCGGCAATAATTCCTATC 480  
QY 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
DB 481 ATCTATGCCTTACTGGGAATTCCTCTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 540  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAen 200  
DB 541 CTAGGCACCATATTGGAAAGAAATGGCAAGTGGAGATACGTTTATTAGTGGAAAT 600  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 601 GTTAGTCAGACCAAGATTCGCATCATCTCACAATCATATTATATATTGGCTGTGTA 660  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 661 CTCTTTTGTGGCTCTGCTGCGATCATATTCAACACATAGAGGCTGGAGTGGCCCTGGAC 720  
QY 241 AlaIleTyThrPheValIleThrLeuThrThrIleGlyPheGlyAspThrValAlaGly 260  
DB 721 GCCATTATTATTGTGGTTATCATCTTAACAACATATTGGATTGGTACACGTTGCAGGT 780  
QY 261 GlySerAspIleGluTyLysLeuAspPheTyLysProValValTrpPheTrpIleLeuVal 280  
DB 781 GGATCCGATATTGAATATCTGGACTCTTATAAGCCCTGTGTGGTGTCTGGATCTTGTGA 840  
QY 281 GlyLeuAlaTyThrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300

DB 841 GGGCTTGGCTTACTTGTCTCTCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 900  
QY 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAen 320  
DB 901 AAAAGACAAAGAGAGAGGTGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCCAC 960  
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyAspLysPhe 340  
DB 961 GTCACAGCCGAATTCAAAGAAACACAGAGGCGACTGAGTGTGGAGATTATGACAAGTTC 1020  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAenHisAenGln 360  
DB 1021 CAGCGGCGCCACTCTCATCAAGCGGAGCTCTCGCAGAGACTGCTGGCAGAACTGGCTGGAACCACTAC 1080  
QY 361 GluLeuThrProCysMetArgThr 368  
DB 1081 GAGCTGACTCTCTTGTAGGAGGACC 1104  
RESULT 5  
AAZ00039  
ID AAZ00039 standard; DNA; 1246 BP.  
XX AAZ00039;  
AC AAZ00039;  
XX 12-OCT-1999 (first entry)  
DT XX  
DE h-TREK1 polynucleotide.  
DE XX  
KW h-TREK1; two pore potassium channel; inflammatory disease;  
KW chromosome 1q32; ss.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 9..1244  
FT /\*tag= a  
FT /\*product= "h-TREK1"  
XX  
PN WO9937762-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 02-DEC-1998; 98WO-EP007805.  
XX  
PR 27-JAN-1998; 98EP-00300570.  
PR 09-OCT-1998; 98GB-00022135.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Meadows HJ, Chapman CG;  
XX  
DR WPI: 1999-469126/39.  
DR P-PSDB; AAY28496.  
XX  
PT New two pore potassium channel used for, e.g. treatment of cancer,  
PT pulmonary, cardiovascular and inflammatory diseases.  
XX  
PS Claim 9; Page 24; 4pp; English.  
XX  
CC This sequence is the h-TREK1 polynucleotide, encoding the h-TREK1  
CC polypeptide AAY28496. h-TREK1 is a two pore potassium channel, and the  
CC gene maps to human chromosome 1q32, between the markers DIS237 and  
CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a  
CC disease or susceptibility to a disease related to expression or activity  
CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
CC treatment of diseases including cancer, pulmonary, cardiovascular, and  
CC inflammatory diseases, pain, psychiatric disorders including depression  
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,  
CC stroke, and head trauma and neurological disorders including migraine  
XX  
SQ Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 U; 0 Other;

Thu Feb 3 07:31:03 2005

Alignment Scores: 7.01e-208 Length: 1246  
 Pred. No.: 1833.00 Matches: 356  
 Score: 98.91% Conservatives: 8  
 Percent Similarity: 96.74% Mismatches: 4  
 Best Local Similarity: 97.34% Indels: 0  
 Query Match: 2 Gaps: 0

US-09-655-272-4 (1-370) x AAZ00039 (1-1246)

QY 1 MetAlaAlaProhepLeuLeuAspProLysSerAlaAlaGlnAsnSerIysProArgLeu 20  
 DB 9 ATGGCGGACCTGACCTGCTGATCTAAATCTGCGCTCGAAGTCCAAACCGAGGCTC 68

QY 21 SerPheSerIysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 DB 69 TCGTTTTCACCAAGAACCCACAGTGTCTTCCGGGTGGAGGTGACACGACCAATTAAT 128

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
 DB 129 GTTATGAATGGAGAGCGTCTCCAGATATCTGCTGTTGCTCTATCTGATCATC 188

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrile 80  
 DB 189 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCCTCATGAGATTTTCAGAGGACCACTT 248

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHiEalaCysValAsnSerThrGluLeuAsp 100  
 DB 249 GTGATCCAGAGCAAAACATTCATATCCCAACATTCCTGTCTCAATTCGACGAGCTGGAT 308

QY 101 GluLeuLeuGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyValSer 120  
 DB 309 GAATCATTCAGCAATAGTGGCAGCAATAAATCAGCGGATTTACCGTTAGGAACACC 368

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerPhePheAlaGlyThrValIle 140  
 DB 369 TCCAAATCAATCAGTCACTGGGATTTGGAGTTTCTTCTTCTTCTTCTTCTTCTTCTT 428

QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160  
 DB 429 ACAACCATAGGATTTGGAAACATCTCACCGCAGAGCGGCAAAATATTTCTGTATC 488

QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 489 ATCTATGCTTACTGGGAATTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 548

QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 549 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGAAGATACGTTTATTAAGTGAAT 608

QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheLeuPheGlyCysVal 220  
 DB 609 GTTAGTCAGACCAAGATTCGCATCATCTCAACATCATATTTATTAATTTGGCTGTGA 668

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 669 CTCTTTGTGCTCTGCTCGCATATTCATCAACATAGAGGCTGGAGTGCCTGGAC 728

QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 729 GCCATTTATTTTGTGTTATCTACTTAAACATTTGGATTTGGTGGATCGTTCAGGT 788

QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 789 GGATCCGATTAATGAAATCTGGACTTCTATAGCCCTGCTGCTGTTCTGGATCTTCTGA 848

QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 849 GGGCTTGTCTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908

QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 909 AAAAAGACAAAAGAGGTGGAGAGTTTCAGAGCACACGCTGCTGCTGCTGCTGCTGCTGCT 968

QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
 DB 969 GTCAAGCCGAAATTCAGAGAACACAGAGGCGACCTGAGTGTGAGATTTATCACAAGTTC 1028

QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisGln 360  
 DB 1029 CAGGGGCGACCTCCATCAAGCGGAAGCTCTCGGCAGAACTCGCTGGAAACCAATCAG 1088

QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1089 GAGCTGACTCTCTTGTAGGAGGACC 1112

RESULT 6  
 AAC90412  
 ID AAC90412 standard; cDNA; 1246 BP.  
 XX  
 AC AAC90412;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Human TREX coding sequence.  
 XX  
 KW Human; TREK; 2P domain potassium channel; resting membrane potential;  
 KW neuronal excitability; neurotransmitter release modulation; epilepsy;  
 KW neurological disorder; sleep-related disorder; cognitive dysfunction;  
 KW attention deficit disorder; addition; anxiety; phobia;  
 KW Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;  
 KW erectile dysfunction; alopecia; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200072863-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 01-JUN-2000; 2000WO-GB002107.  
 XX  
 PR 01-JUN-1999; 99GB-00012733.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Hervieu GJ, Meadows HJ, Randall AD;  
 DR WPI; 2001-080422/09.  
 DR P-PSDB; AAB50044.  
 XX  
 PT Use of human TREK1 polypeptide, polynucleotides encoding them and  
 PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
 PT disorders, addiction and dyskinesias including Parkinson's and  
 PT Huntington's chorea.  
 XX  
 PS Claim 12; Page 29; 35pp; English.  
 XX  
 CC The present sequence is the coding sequence for human TREK1 (h-TREK1). h-  
 CC TREK1 is a member of the 2P domain potassium channel family of proteins  
 CC which play a part in the control of resting membrane potential.  
 CC Modulation of these channels will therefore affect neuronal excitability,  
 CC thereby leading to a modulation of neurotransmitter release and activity  
 CC of neuronal networks. Such modulation therefore may be useful for the  
 CC treatment of certain neurological conditions such as epilepsy, sleep-  
 CC related disorders, cognitive dysfunction, attention deficit disorder,  
 CC addition, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral  
 CC palsy, incontinence, erectile dysfunction or alopecia  
 XX  
 SQ Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 U; 0 Other;

Alignment Scores: 7.01e-208 Length: 1246  
 Pred. No.: 1833.00 Matches: 356  
 Score: 98.91% Conservatives: 8  
 Percent Similarity: 96.74% Mismatches: 4  
 Best Local Similarity: 97.34% Indels: 0  
 Query Match:

DB:	4	Gaps:	0
US-09-655-272-4 (1-370) x AAC90412 (1-1246)			
QY	1	MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu	20
Db	9	ATGGCGGCACCTGACTTGTGGATCTTAATCTGCCGCTCAGAACTCCAAACCGAGGCTC	68
QY	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	69	TCGTTTCCACGAAACCCACAGTCTTCTCCCGGTGGAGAGTGACACGACCAATTAAT	128
QY	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValIleIle	60
Db	129	GTATGAAATGGGAAGCGGTCTCCAGATATCTCGTGGTGTCTCTATCTGATCATC	188
QY	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle	80
Db	189	GGAGCCACCGTGTTCAGCATTTGGAGCAGCCTCATGAGATTTTCACAGGAGCACCAT	248
QY	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
Db	249	GTGATCCAGAAGCAACATTCATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT	308
QY	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
Db	309	GAATCTATTGAGCAAAATAGTGGCAGCAATAAATGCGAGGATTTATACCGTTAGGAAAC	368
QY	121	SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140
Db	369	TCCAAATCAATAGTCACTGGGATTTGGGAAGTTCCTTCTTCTGGCATCTGTATT	428
QY	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle	160
Db	429	ACAACCATAGGATTTGGAAACATCTCCACGACACAGAGCGCGCAATAATTCGTATC	488
QY	161	IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
Db	489	ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG	548
QY	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	549	CTAGGCACCATATTGGAAAGGAATTCGCAAGTGGAGATGAGTTTATAGTGGAAAT	608
QY	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	609	GTATAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATCTATTTGCTGTGA	668
QY	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	669	CTCTTTGTGGCTCTGCTGCGATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC	728
QY	241	AlaIleTyPheValValIleThrLeuThrThrIleGlyPheGlyAspTyValAlaGly	260
Db	729	GCCATTTATTTGTGGTATCATCTTAACAACATTTAGATTTGGTACACGTGTGAGGT	788
QY	261	GlySerAspIleGluTyLeuAspPheTyLysProValValTrpPheTrpIleLeuVal	280
Db	789	GGATCCGATATTCGAATCTCGACTTATACGCTGTCTGCTGGTTCGATCCTTGTGA	848
QY	281	GlyLeuAlaTyPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
Db	849	GGGCTTGTCTTACTTGTCTGCTGCTGATGATGATGGATGGCTCCGAGTATATCT	908
QY	301	LysLeuThrLysGluGluValGlyPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320
Db	909	AAAAAGACAAAGAGAGTGGAGAGTTTCAGAGCACACCTCTGAGTGACAGGCAAC	968
QY	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyAspLysPhe	340
Db	969	GTACAGCCGCAATTCAAAGAAACAGGAGCGGCTGAGTGTGAGATTTATGACAGTTC	1028
QY	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln	360

Db	1029	CAGCGGCGCACCTTCATCAAGCGGAGCTCTCGCGAGAACTGGCTGGAAACCAATCAG	1088
QY	361	GluLeuThrProCysMetArgThr	368
Db	1089	GAGCTGACTCTCTGTAGGAGGACC	1112
RESULT 7			
AAZ11915			
ID	AAZ11915	standard; cDNA; 3300 BP.	
XX	AAZ11915;		
AC	AAZ11915;		
XX	30-NOV-1999	(first entry)	
DT			
XX	Human potassium channel K-Hnov59 cDNA.		
DE			
XX	Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;		
KW	cardiovascular disorder; CNS disorder; renal disorder; ds.		
XX	Homo sapiens.		
OS			
XX	Key	Location/Qualifiers	
PH	CDS	50..1285	
FT		/tag= a	
FT		/product= "Human K-Hnov59 potassium channel"	
XX	WO9943696-A1.		
PN			
XX	02-SEP-1999.		
PD			
XX	22-FEB-1999;	99WO-US003826.	
PF			
XX	25-FEB-1998;	98US-0076687P.	
PR			
XX	07-AUG-1998;	98US-0095836P.	
PR			
XX	19-JAN-1999;	99US-0116448P.	
PA			
XX	(AXYS-) AXYS PHARM INC.		
PI	Miller AP, Curran ME, Hu P, Rutter M, Wang J;		
XX	WPI: 1999-527591/44.		
DR	P-PSDB; AAY34133.		
XX	New nucleic acids encoding mammalian K-Hnov potassium channel proteins,		
PT	useful for the diagnosis and treatment of episodic ataxia with myokymia,		
PT	cardiac arrhythmia, epilepsy and Bartter's syndrome.		
XX	Claim 4; Page 102-104; 112pp; English.		
PS			
XX	This sequence represents human potassium channel K-Hnov59 cDNA. K-Hnov		
CC	proteins have a high degree of homology to known potassium channels and		
CC	may be alpha subunits, which form the functional channel, or accessory		
CC	subunits that act to modulate the channel activity. K-Hnov59 is a 4		
CC	transmembrane domain, 2 pore domain potassium channel. The gene is		
CC	located on chromosome 19, determined via PCR chromosomal localisation		
CC	using primers AAZ11939 and AAZ11940. K-Hnov cDNAs were isolated by		
CC	extension of expressed sequence tags (ESTs) which were related but not		
CC	identical to known human potassium channels. Potential polymorphisms		
CC	detected as sequence variants between multiple independent clones.		
CC	Potassium channels have critical roles in various cell types and		
CC	biochemical pathways. Defective potassium channels are known to cause		
CC	four human diseases: episodic ataxia with myokymia; cardiac arrhythmia		
CC	(long QT syndrome); epilepsy; and Bartter's syndrome. As potassium		
CC	channels are critical components of virtually all cells, it is likely		
CC	that abnormal potassium channels are also implicated in certain renal,		
CC	cardiovascular and central nervous system (CNS) disorders. Nucleotides		
CC	encoding K-Hnov proteins may be used for identifying homologous or		
CC	related proteins and the DNA sequences encoding them. They may be used to		
CC	produce compositions that modulate the expression and function of the		
CC	K-Hnov protein and in studying the biochemical pathways associated with		
CC	it. They may also be used for the recombinant production of K-Hnov		
CC	protein in fermentation cultures. Additionally, such nucleotides may be		

XX The invention relates to a novel isolated GPCR (G-protein coupled  
CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of  
CC the invention demonstrate neuroprotective, nootropic, tranquiliser,  
CC antismigraine, neuroleptic, antianemic, antidepressant, anticonvulsant,  
CC

CC antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal,  
 CC analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,  
 CC antiulcer and antiallergic properties. The nucleic acid molecule and  
 CC polypeptide of the invention may be useful in diagnosing, preventing,  
 CC treating or ameliorating a medical condition, such as a disorder related  
 CC to aberrant G-protein coupled signalling, a disorder related to aberrant  
 CC cell cycle regulation, neurological disorders, severe mental retardation  
 CC and dyskinesias, brain disorders, spinal cord disorders, affective  
 CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
 CC disorders, immune-related disorders, endocrinal diseases, growth  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor) DNA  
 CC which was isolated by the method of the invention.

SQ Sequence 2391 BP; 662 A; 503 C; 537 G; 689 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 9.81e-207 Length: 2391  
 Score: 1827.00 Matches: 354  
 Percent Similarity: 98.91% Conservative: 10  
 Best Local Similarity: 96.20% Mismatches: 4  
 Query Match: 97.03% Indels: 0  
 DB: 11 Gaps: 0

US-09-655-272-4 (1-370) x ADP03564 (1-2391)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 586 TTGGCGGCACCTGACTTGGTGGATCTCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 645  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 DB 646 TCGTTTCCAGAAACCCACAGTGTCTTCCGGGTGGAGTGCACGACCATTAAT 705  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
 DB 706 GTTATGAATGGAAGACGGTCTCCACGATATCTCTGGTGTCTCTCTATCTGATCATC 765  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
 DB 766 GGAGCCACCGTGTCAAGACATTTGGAGCAGCCCTCATGAGATTTTCACAGAGGACCACT 825  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 826 GTGATCCAGAGCAACATTCATATCCCAACATCTCTGTCTCAATTCGACGGAGCTGGAT 885  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 886 GAACTCATTGAGCAATAGTGGCAGCAATAAATGCAGGGATATATCCGTTAGGAAACACC 945  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 946 TCCAATCAATAGTCACTGGGATTTGGGAAGTTCCTTCTTCTGCTGGCACTGTATT 1005  
 QY 141 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 DB 1006 ACAACCATAGGATTTGGAAACATCTCACACGACACAGAGCGGCAAAATATCTGTATC 1065  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 1066 ATCTATGCCCTACTGGGAATTCCTTTGGTCTTCTCTGGCTGGAGTTGGAGATCAG 1125  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 1126 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAAAGTACGTTTATTAAGTGAAT 1185  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 1186 GTTAGTCAGACCAAGATTCCATCTCATCTCAACATCATATTTTACTATTTGGCTGTGTA 1245

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 1246 CTCCTTTGTGGCTCTGCTGCGATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC 1305  
 QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 1306 GCCATTTATTTGTGGTTATCACTCTTAACACTATTGGATTGGTGTGACTACGTTGACGGT 1365  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 1366 GGATCCGATATTGAATATCTGGACTTCTATAAGCCCTGTGCTGTGTTCTGGATCCTTGTGA 1425  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1426 GGGCTTGTCTTACTTGTCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 1485  
 QY 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1486 AAAAAACAAGAGAGGTGGAGAGTTCAAGACACGCTGCTGAGTGACAGCCAC 1545  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe 340  
 DB 1546 GTCACAGCCGAAATTCAAGAAACACAGAGCGGACTGAGTGTGGAGATTTATGACAAAGTTC 1605  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1606 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAGAACTGCTGGAAACCAATCATG 1665  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1666 GAGCTGACTCTTGTAGGAGGACC 1689  
 RESULT 9  
 AAS12169  
 ID AAS12169 standard; cDNA; 2130 BP.  
 XX AAS12169;  
 AC AAS12169;  
 DT 21-NOV-2001 (first entry)  
 XX Human potassium ion channel TPKC1 cDNA.  
 DE Transmembrane potassium ion channel protein; inward potassium flux; as;  
 XX pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 178..1458  
 FT /\*tag= a  
 FT /product= "Human TPKC1 protein"  
 XX  
 PN W0200161006-A2.  
 XX  
 XX 23-AUG-2001.  
 PD  
 XX 14-FEB-2001; 2001WO-US004680.  
 XX  
 XX 15-FEB-2000; 2000US-00503849.  
 XX  
 XX (BADI ) BASF CORP.  
 PA  
 XX Pausch MH;  
 XX  
 XX WPI; 2001-536570/59.  
 DR P-PSDB; AAU07618.  
 DR  
 XX New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.  
 XX  
 XX Example 15; Page 45-46; 131pp; English.  
 PS  
 XX

CC The invention relates to a mutant potassium ion channel protein, having a  
CC four membrane spanning domains and two pore forming domains, comprising a  
CC mutation at the second pore forming domain. The expression of the mutant  
CC protein in a cell confers improved inward potassium flux and the ability  
CC to grow in the presence of potassium. Mutant proteins and their  
CC corresponding polynucleotide sequences can therefore be used to improve  
CC inward potassium flux into cells under acidic conditions by modulating  
CC the membrane potential using therapeutic agents. The sequences may be  
CC used to develop agonists and antagonists of potassium channel proteins in  
CC order to control pests such as nematodes and insects. This sequence  
CC represents a human cDNA encoding a transmembrane potassium ion channel  
CC protein, TPCK1  
XX  
SQ Sequence 2130 BP; 564 A; 480 C; 488 G; 593 T; 0 U; 5 Other;

Alignment Scores: 3.44e-204 Length: 2130  
Pred. No.: 1805.00 Matches: 352  
Score: 98.37% Conservative: 10  
Percent Similarity: 98.37% Mismatches: 6  
Best Local Similarity: 95.65% Indels: 0  
Query Match: 95.86% Gaps: 0  
DB:

US-09-655-272-4 (1-370) x AAS12169 (1-2130)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAnSerLysProArgLeu 20  
DB 223 GTGGCGGCACCTGCTGATCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 282  
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
DB 283 TCATTTTCCAGAAACCCACAGTGTCTTCCCGGTGGAGTGCACACGACCATTAAT 342  
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLysLeuIle 60  
DB 343 GTTATGAAATGGAACAGCTCTCCACGATATCTCGTGTGTCTCTATCTGATCATC 402  
QY 61 GlyAlaAlaValPheLysAlaLeuGlnProGlnGluLeuSerGlnArgThrIle 80  
DB 403 GGAGCCACCGTGTTCAGAGCATGGAGCAGCTCATGAGATTCACAGAGCCACCAT 462  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAnSerThrGluLeuAsp 100  
DB 463 GTGATCCAGAGCAACATTCATATCCCAACATCTCTGTCAATTCAGCGAGCTGGAT 522  
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAlaGlyIleIleProLeuGlyAnSer 120  
DB 523 GAACATCATTCAGCAATAGTGGCAGCAATAAATGAGGAGTATACCTTTAGGAAACACC 582  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 583 TCCAAATCAATACAGTCACTGGGATTTGGGAGTCTCTTCTTCTTGGCAGCTGTATT 642  
QY 141 ThrThrIleGlyPheGlyAsnLeuSerProArgThrGluGlyGlyIlePheCysIle 160  
DB 643 ACAACCATAGATTTGGAAACATCTCACCACGCACAGAGCGGCAAAATATCTGTATC 702  
QY 161 IleTyraLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180  
DB 703 ATCTATGCCCTTACTGGGAATTTCCCTCTTTGGTTTCTTCTTGGCTGGAGTTGAGATCAG 762  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAn 200  
DB 763 CTAGGCACCATATTTTGGAAAGGAATTTGCCAAAGTGAAGATACGTTTAAAGTGAAT 822  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 823 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATATTTCCTGTGTA 882  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 883 CTCCTTTGGCTCTGGCTGCATATTTCAAAACATAGAGGCTGGAGTGCCTGGAC 942

QY 241 AlaIleTyraPheValValIleThrLeuThrThrIleGlyPheGlyAspTyraValAlaGly 260  
DB 943 GCCATTTATTTTGTGTATCACTCTAAACAATTTGGTACTTACCTTGCAGGT 1002  
QY 261 GlySerAspIleGluTyraLeuAspPheTyraLysProValValTrpPheTrpIleLeuVal 280  
DB 1003 GGATCCGATATTGAATATCTGGACTTCTATAAGCCCTGTCTGTGGTCTTGGATCCTGTA 1062  
QY 281 GlyLeuAlaTyraPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
DB 1063 GGGCTTCTTACTTGTCTGTCTCTGAGCATGATTTGGGAGATTTGTCGAGTGATATCT 1122  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGlnTrpThrAlaAsn 320  
DB 1123 AAAAAGACAAAAGAGAGGTGGGAGATTTCAGAGCACACGCTCTGAGTGGACGCAAC 1182  
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyraAspLysPhe 340  
DB 1183 GTCACGCCGAATTCAAAGAAACCCAGAGGCGACTGAGTGTGGAGATTTATGACAAAGTTC 1242  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1243 CAGCGGCCACCTCATCAAGCGGAGCTCTCGCAGAACTCTCGCAGAACTGGCTGGAAACCAATCAG 1302  
QY 361 GluLeuThrProCysMetArgThr 368  
DB 1303 GAGCTGACTCTTGTAGGAGACC 1326  
RESULT 10  
AAS12181  
ID AAS12181 standard; cDNA; 2130 BP.  
XX AAS12181;  
XX 21-NOV-2001 (first entry)  
DT Human potassium ion channel protein TPCK1 cDNA mutant #1.  
DE Transmembrane potassium ion channel protein; inward potassium flux; ss;  
KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
KW insect; TPCK1; human; mutant.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
CDS 178..1458  
FT /\*tag= a  
FT /\*product= "Human TPCK1 mutant protein #1"  
FT mutation replace(943,G)  
FT /\*tag= b  
XX WO200161006-A2.  
XX 23-AUG-2001.  
XX 14-FEB-2001; 2001WO-US0004680.  
XX 15-FEB-2000; 2000US-00503849.  
XX (BADI ) BASF CORP.  
XX Pausch MH;  
XX WPI: 2001-536570/59.  
XX P-PSDB; RAU07622.  
XX New polypeptide, a mutant potassium ion channel protein for improving  
XX inward potassium flux under acidic conditions.  
XX Claim 12; Page 121-122; 131pp; English.  
XX The invention relates to a mutant potassium ion channel protein, having a  
XX four membrane spanning domains and two pore forming domains, comprising a





CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human cDNA encoding a transmembrane potassium ion channel  
 CC mutant TPKC1 protein  
 XX  
 SQ Sequence 2130 BP; 564 A; 481 C; 488 G; 592 T; 0 U; 5 Other;

Alignment Scores: 1.36e-203 Length: 2130  
 Pred. No.: 1800.00 Matches: 351  
 Percent Similarity: 98.37% Conservative: 11  
 Best Local Similarity: 95.38% Mismatches: 6  
 Query Match: 95.59% Indels: 0  
 DB: 4 Gaps: 0

US-09-655-272-4 (1-370) x AAS12182 (1-2130)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu 20  
 DB 223 GTGGGGGACCTGACTGCTGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 282  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerSerAlaIleAsn 40  
 DB 283 TCATTTTCCAGAAACCCACACAGTCTTGCCTTCCGGGTGGAGAGTGACAGACANTTAT 342  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuThrLeuIle 60  
 DB 343 GTTATGAATGGAGACGGTCTCCAGCATATCTGCTGGTGTCTCTATCTGATCATC 402  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
 DB 403 GGAGCCACCGTGTTCAGAGCATTTGAGCAGCCTCATGAGATTTCCAGAGACCCACAT 462  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp 100  
 DB 463 GTGATCCAGAGCAAAACATTCATATCCCAACATTCCTGTGTCAATTCAGAGAGCTGAT 522  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAenAlaGlyIleIleProLeuGlyAenSer 120  
 DB 523 GAATCATTCAGCAATAGTGGCAGCAATAAATGCGGATATATACCGTTAGGAACACC 582  
 QY 121 SerAenGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 583 TCCAATCAATCAGTCACCTGGGATTTGGGAAGTTCCTTCTTCTGCGGACCTGTATT 642  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160  
 DB 643 ACACCATAGGATTTGGAAACATCTCACCGCAGAGAGCGGCAAAATATTTCTGTATC 702  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValClyAspGln 180  
 DB 703 ATCTATGCTTACTGGGAATTCCTCTTTGTTTCTCTGCGTGGAGTTGGAGATCAG 762  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 763 CTAGGCACCATATTTGGAAAGGATTTGCCAAGTGGAGAGATACGTTATTAAAGTGAAT 822  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 DB 823 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATATTTCGCTGTGTA 882  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 883 CTCTTTTGGCTCTGCTGCGATCATATTCAAACATAGAGCTGGAGTCCCTGGAC 942  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 943 GCCATTATTTTGGTGTATCACTCTCAACATATTGGATTGTTGGTACCACCGTTGAGGT 1002

QY 261 GlySerAspIleGluTyrIleuAspPheTyrLysProValValTrpPheTrpIleuVal 280  
 DB 1003 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGCTGCTGGTTCCTTGA 1062  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1063 GGGCTTGCTTACTTGTCTGCTGCTGAGCATATTGGAGATTGGTCCGAGTGATATCT 1122  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1123 AAAAGAACAAGAGAGGTGGAGATTTCAGAGCACACGCTGCTGAGTGGACAGCAAC 1182  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe 340  
 DB 1183 GTACAGCCGAATTCAAAGAAACACAGAGGCGACTGAGTGTGGAGATTATGACAAAGTTC 1242  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAenHisAenGln 360  
 DB 1243 CAGCGGGCCACCTCCATCAACGGAGAGCTCTCGGAGAACTGGCTGGAAACCAACATCAG 1302  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1303 GAGCTGACTCTTGTAGGAGGACC 1326  
 RESULT 12  
 AAS12184  
 ID AAS12184 standard; cDNA; 2130 BP.  
 XX AAS12184;  
 AC AAS12184;  
 XX 21-NOV-2001 (first entry)  
 DT Human potassium ion channel protein TPKC1 cDNA mutant #4.  
 DE Transmembrane potassium ion channel protein; inward potassium flux; ss;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human; mutant.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 PH 178.1458  
 CDS /\*tag= a  
 FT /product= "Human TPKC1 mutant protein #4"  
 FT replace(985,G)  
 FT mutation /\*tag= b  
 FT WO200161006-A2.  
 XX  
 XX PD 23-AUG-2001.  
 XX  
 XX PF 14-FEB-2001; 2001WO-US004680.  
 XX  
 XX PR 15-FEB-2000; 2000US-00503849.  
 XX  
 XX PA (BADI ) BASF CORP.  
 XX  
 XX FI Pausch MH;  
 XX  
 XX DR WPI; 2001-536570/59.  
 XX DR P-PSDB; AAU07625.  
 XX  
 XX PT New polypeptide, a mutant potassium ion channel protein for improving  
 XX inward potassium flux under acidic conditions.  
 XX  
 XX PS Claim 12; Page 126-127; 131pp; English.  
 XX  
 XX The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve



CC inward potassium flux into cells under acidic conditions by modulating  
CC the membrane potential using therapeutic agents. The sequences may be  
CC used to develop agonists and antagonists of potassium channel proteins in  
CC order to control pests such as nematodes and insects. This sequence  
CC represents a human cDNA encoding a transmembrane potassium ion channel  
CC mutant TPB1 protein  
XX  
SQ Sequence 2130 BP; 564 A; 480 C; 488 G; 593 T; 0 U; 5 Other;

Alignment Scores: 4.07e-203 Length: 2130  
Pred. No.: 1796.00 Matches: 350  
Score: 98.10% Conservative: 11  
Percent Similarity: 95.11% Mismatches: 7  
Best Local Similarity: 95.11% Indels: 0  
Query Match: 95.38% Gaps: 0  
DB: 4

US-09-655-272-4 (1-370) x AAS12183 (1-2130)

Qy	1	MetAlaLapProApLeuLeuAAspProLysSerAlaAlaGlnAenSerLysProArgLeu	20
Db	223	GTGGCGGACCTGACTTGGTGGATCTTAATCTGCCGCTCAGAACTCCAAACCGAGCTC	282
Qy	21	SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	283	TCATTTTCCAGAAACCCACAGTCTTGGCTTCCCGGGTGAGAGTGACACGACCATTAAT	342
Qy	41	ValMetLysThrLysThrValSerThrIlePheLeuValValValLeuTyrLeuIleIle	60
Db	343	GTATGAATGGAAGACGGTCTCCACGATATTCCTGGTGGTGTCTCTATCTGATCATC	402
Qy	61	GlyAlaAlaValPheLysAlaLeuGluLapProGlnLysSerGlnArgThrThrIle	80
Db	403	GGAGCCACCGGTTCAAAGCATTGGAGCAGCTCATGAGATTTCACAGAGACCACTT	462
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp	100
Db	463	GTGATCCAGAGCAACATTCATATCCCACTTCTGTGTCATTCGACGGAGCTGGAT	522
Qy	101	GluLeuIleGlnGlnIleValAlaAlaIleAenAlaGlnIleIleProLeuGlyAenSer	120
Db	523	GAACCTCAATTCAGCAATAGTGGCAATTAATGCGGGATTATACCGTTAGGAAACACC	582
Qy	121	SerAenGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140
Db	583	TCCATCAATCAGTCATCTGGATTGGGAAGTTCCTTCTTCTTGGCACTGTATT	642
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160
Db	643	ACAACCATAGGATTTGGAACAATCTCACCGCACAGAGCGGCAAAATATTCTGTATC	702
Qy	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
Db	703	ATCTATGCTTACTGGGAATCCCTCTTGTGTTTCTTGGCTGGAGTTGGAGATCAG	762
Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	763	CTAGGCACCATATTGGAAAGGAATTCGAAAGTGAAGATACGTTTATTAAAGTGAAT	822
Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	823	GTATGTCAGACCAAGATTCGCATCATCTCAACAATCATATTATATATTGGCTGTGTA	882
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	883	CTCTTTGTGGCTCTGCTGCGATCATATTCAACACATAGAGGCTGGAGTCCCTGGAC	942
Qy	241	AlaIleTyrPheValValIleThrThrIleGlyPheGlyAspTyrValAlaGly	260
Db	943	GCAATTTATTTTGTGTTATCACTCTAAACAATATTGGATTGGTGACCACTGTAGGT	1002
Qy	261	GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal	280

Db	1003	GGATCCGATATTGAATATCTGGACTTCTATTAAGCCTGTCTGTTGGTCTCTGGATCCTTTGTA	1062
Qy	281	GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
Db	1063	GGGCTTGTCTTACTTGTCTGTCTCTGATGATTTGGGAGATTGGTCCGAGTGATATCT	1122
Qy	301	LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTyrThrAlaAsn	320
Db	1123	AAAAAGACAAAGAGAGGTGGAGAGTTTCAGACACACACCTGCTGAGTGACAGCCAAC	1182
Qy	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe	340
Db	1183	GTCAAGCCGGAATTCAAAGAAACCCAGAGGCGCATCTGAGTGTGGAGATTATGACAGTTC	1242
Qy	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln	360
Db	1243	CAGCGGGCCACTCCATCAAGCGGAAGCTCTCGGAGAACTGGCTGGAAACCAATCAG	1302
Qy	361	GluLeuThrProCysMetArgThr	368
Db	1303	GAGCTGACTCCTTGTAGGAGGACC	1326
RESULT 14.			
ID	ACC46425	standard; cDNA; 3393 BP.	
XX	ACC46425;		
DT	02-JUN-2003	(first entry)	
DE	Human dithp membrane transport protein-encoding cDNA.		
XX	Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;		
KW	cancer; cell proliferative disorder; autoimmune disorder;		
KW	inflammatory disorder; infection; hormonal disorder; metabolic disorder;		
KW	neurological disorder; gastrointestinal disorder; transport disorder;		
KW	connective tissue disorder; drug screening; proteome analysis;		
KW	gene therapy; antisense therapy; genotyping; transgenic animal; knock in;		
KW	disease model; toxicological testing; transcript imaging;		
KW	membrane transport protein; gene; ss.		
OS	Homo sapiens.		
XX	WO200297031-A2.		
XX	05-DEC-2002.		
XX	27-MAR-2002; 2002WO-US010056.		
XX	28-MAR-2001; 2001US-0279619P.		
PR	29-MAR-2001; 2001US-0280067P.		
PR	29-MAR-2001; 2001US-0280068P.		
PR	16-MAY-2001; 2001US-0291280P.		
PR	17-MAY-2001; 2001US-0291829P.		
PR	17-MAY-2001; 2001US-0291849P.		
PR	19-JUN-2001; 2001US-0299428P.		
PR	20-JUN-2001; 2001US-0299776P.		
XX	20-JUN-2001; 2001US-0300001P.		
XX	(INCY-) INCYTE GENOMICS INC.		
XX	Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;		
PI	Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Anshey SR;		
PI	Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;		
PI	Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;		
PI	Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;		
DR	WPI: 2003-129518/12.		
DR	P-PSDB; ABR41487.		
XX	Novel human diagnostic and therapeutic polypeptide useful for identifying		
PT	test compound which specifically binds to a polypeptide encoded by human		
PT	diagnostic and therapeutic polynucleotide, and to induce antibodies.		

XX PS Claim 2; SEQ ID NO 346; 591pp; English.

XX CC The invention relates to novel human diagnostic and therapeutic

CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded

CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to

CC polynucleotide sequences at least 90% identical to the dithp cDNA

CC sequences of the invention; recombinant vectors, host cells and

CC transgenic organisms comprising a dithp nucleic acid sequence; the

CC recombinant production of DITHP proteins; antibodies specific for DITHP

CC proteins; microarrays comprising dithp nucleic acid sequences; methods of

CC detecting dithp nucleotide and protein sequences; methods of screening

CC for compounds which specifically bind a DITHP protein; and methods of

CC assessing the toxicity of test compounds using a dithp hybridisation

CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the

CC diagnosis of a wide variety of conditions including cancer and other cell

CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,

CC viral, fungal or parasitic infections; hormonal disorders; metabolic

CC disorders; neurological disorders; gastrointestinal disorders; transport

CC disorders; and connective tissue disorders. They may also be used to

CC screen for modulators of protein activity or gene expression. DITHP

CC proteins can additionally be used in analysis of the proteome of a tissue

CC or cell type and to induce antibodies. The dithp nucleic acids are

CC additionally useful in somatic or germline gene therapy of the disorders

CC mentioned above, as a source of antisense sequences, as a source of

CC probes and primers, in genotyping and identification of individuals, in

CC the generation of transgenic animal models of human disease or knock in

CC humanised animals, in toxicological testing, and in transcript imaging.

CC The present sequence represents a dithp cDNA encoding a DITHP protein

CC which has membrane transport protein activity. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 3393 BP; 978 A; 667 C; 716 G; 1032 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.49e-196 Length: 3393

Score: 1743.50 Matches: 351

Percent Similarity: 97.83% Conservative: 9

Best Local Similarity: 95.38% Mismatches: 8

Query Match: 92.59% Indels: 4

DB: 8 Gaps: 0

US-09-655-272-4 (1-370) x ACC46425 (1-3393)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20

DB 188 GTGGCGGACCTGACTTGTCTGGATCTTAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 247

QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40

DB 248 TCATTTTCCAGAAACCCACAGCTGTCTTCCCGGTGGAGAGTGACACGACCATTAAT 307

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTrpLeuIleIle 60

DB 308 GTTATGAATGGAAGACGGTCTCCAGATATTCTCTGGTGGTGTCTCTATCTGATCATC 367

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80

DB 368 GGAGGCCACCGTGTTCAAAGCATTTGGAGCAGCTTCATGAGATTTCACAGAGGACCATTT- 426

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100

DB 427 GTGATCCAGAGCA-ACATTTCATATCCCA-CATTCTCTGTGTCTAT-TCGACGGAGCTGGAT 483

QY 101 GluLeuIleGlnGlnIleValAlaIleAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120

DB 484 GAACTCATTCAGCAATAGTGGCAGCAATAAATGAGGGATTATACCGTTAGGAAACACC 543

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140

DB 544 TCCAAATCAATCAGTCACCTGGGATTGGGAAGTTCCTTCTTTGCTGGCAGCTGTATT 603

QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160

DB 604 ACAACCAATAGGATTGGAAACATCTCACACGACACAGAGGGCGGAAAAATATTCTGTATC 663

QY 161 IleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180

DB 664 ATCTATGCTTACTGGGAATTCCTCTTTGGTTTCTCTGGCTGGAGTTGGAGATCAG 723

QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200

DB 724 CTAGGCACCATATTGGAAAGGAATTCGCAAGTGAAGATACGTTTATTAAAGTGAAT 763

QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220

DB 784 GTTAGTCAGACCAAGATTGCGCATCTCTCAACAATCATATTTATATTATTTGGCTGTGA 843

QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240

DB 844 CTCCTTTGTGGCTCTCGCTGCGATCATATTCAACACATAGAAGCTGGAGTGGCCCTGGAC 903

QY 241 AlaIleTrpPheValValIleThrLeuThrIleGlyPheGlyAspTrpValAlaGly 260

DB 904 GCCATTATTTTGTGGTTATCACTCTAACAACTATTGGATTGGTACCTACGTTGCAGGT 963

QY 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal 280

DB 964 GGATCCGATATTGAATATCTGGACCTCTATAAGCCCTGCTGCTGGTTCCTGGATCCTTGA 1023

QY 281 GlyLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300

DB 1024 GGGCTGTGCTTACTTGTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 1083

QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320

DB 1084 AAAAGACAAAAGAGAGGTGGAGATTTCAGACACACGCTGCTGAGTGGACGCCAAC 1143

QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTrpAspLysPhe 340

DB 1144 GTCACAGCCGAATTCAAAGAAACAGGAGGCTGAGTGTGGAGATTATGACAAAGTTC 1203

QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyHisAsnGln 360

DB 1204 CAGCGGGCCACTCCATCAAGCGGAAGCTCTCGGAGAACTGGCTGGAAACCAATCAG 1263

QY 361 GluLeuThrProCysMetArgThr 368

DB 1264 GAGCTGACTCTCTTGTAGGAGGACC 1287

RESULT 15

ADJ27238

ID ADJ27238 standard; DNA; 1702 BP.

XX AC ADJ27238;

XX AC ADJ27238;

DT 20-MAY-2004 (first entry)

XX DE Human TRICH-22 coding sequence, SEQ ID 70.

XX KW Human; Transporters and Ion Channels protein; TRICH; Transporter;

KW Ion Channel; transport disorder; neurological disorder; muscle disorder;

KW Immunological disorder; cell proliferative disorder; infection;

KW Neuroprotective; Muscular; Respiratory; Antidiabetic; Antiparkinsonian;

KW Nootropic; Anticonvulsant; Antithyroid; Ophthalmological; Antibacterial;

KW Antiinflammatory; Cardiant; Anti-anginal; Antiarrhythmic; Antiasthmatic;

KW Endocrine; Hypotensive; Anti-HIV; Antianemic; Antiarteriosclerotic;

KW Dermatological; Antiarthritic; Osteopathic; Antipruritic; Antirheumatic;

KW Immunosuppressive; Anticancer; Gastrointestinal; Hepatotropic; Cystostatic;

KW Virucide; Fungicide; Antiparasitic; Protozoacide; Antihelminthic;

KW Gene Therapy; TRICH-22; gene; ds.

XX OS Homo sapiens.

XX XX



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 22:01:01 ; Search time 99.7266 Seconds  
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Title: US-09-655-272-4

Perfect score: 1883

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1870	99.3	1994	3	US-09-236-080-5
2	1833	97.3	1246	3	US-09-236-080-1
3	1833	97.3	3700	3	US-09-336-643A-82
4	1247.5	66.3	2730	4	US-09-799-451-432
5	797	42.3	1182	4	US-09-432-470-1
6	797	42.3	1218	4	US-09-432-470-3
7	797	42.3	3996	4	US-09-620-312D-195
8	547	29.0	321	3	US-09-236-080-3
9	416.5	22.1	1497	4	US-09-561-763-3
10	416.5	22.1	1497	4	US-09-431-367B-3
11	416.5	22.1	3452	4	US-09-561-763-1
12	416.5	22.1	3452	4	US-09-431-367B-1

13	397.5	21.1	1086	4	US-09-362-842-13	Sequence 13, Appl
14	387	20.6	996	4	US-09-561-763-6	Sequence 6, Appl
15	387	20.6	996	4	US-09-431-367B-6	Sequence 6, Appl
16	387	20.6	1575	4	US-09-561-763-4	Sequence 4, Appl
17	387	20.6	1575	4	US-09-431-367B-4	Sequence 4, Appl
18	378.5	20.1	2514	3	US-09-144-914-3	Sequence 3, Appl
19	377	20.0	1882	4	US-09-814-915A-45	Sequence 45, Appl
20	377	20.0	1894	3	US-08-749-816-1	Sequence 1, Appl
21	377	20.0	1894	3	US-09-144-914-1	Sequence 1, Appl
22	342	18.2	939	4	US-09-561-763-9	Sequence 9, Appl
23	342	18.2	939	4	US-09-431-367B-9	Sequence 9, Appl
24	342	18.2	2287	4	US-09-561-763-7	Sequence 7, Appl
25	342	18.2	2287	4	US-09-431-367B-7	Sequence 7, Appl
26	342	18.2	2571	3	US-09-336-643A-80	Sequence 80, Appl
27	317.5	16.9	1227	4	US-09-362-842-11	Sequence 11, Appl
28	315	16.7	2441	1	US-08-332-312-1	Sequence 1, Appl
29	256.5	13.6	1188	4	US-09-362-842-5	Sequence 5, Appl
30	219	11.6	1011	1	US-08-332-312-3	Sequence 3, Appl
31	216.5	11.5	2193	4	US-09-362-842-3	Sequence 3, Appl
32	212	11.3	1203	4	US-09-561-763-12	Sequence 12, Appl
33	212	11.3	1203	4	US-09-431-367B-12	Sequence 12, Appl
34	212	11.3	1506	4	US-09-561-763-10	Sequence 10, Appl
35	212	11.3	1506	4	US-09-431-367B-10	Sequence 10, Appl
36	211	11.2	2288	4	US-09-362-842-1	Sequence 1, Appl
37	203.5	10.8	3033	4	US-09-362-842-66	Sequence 66, Appl
38	203.5	10.8	3033	4	US-09-270-767-13872	Sequence 13872, A
39	174.5	9.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
40	174.5	9.3	1664976	4	US-09-692-570-1	Sequence 1, Appl
41	172	9.1	3462	4	US-09-362-842-7	Sequence 7, Appl
42	162.5	8.6	923	3	US-09-336-643A-15	Sequence 15, Appl
43	141	7.5	438	4	US-09-362-842-68	Sequence 68, Appl
44	141	7.5	438	4	US-09-270-767-56	Sequence 56, Appl
45	141	7.5	438	4	US-09-270-767-15338	Sequence 15338, A

#### ALIGNMENTS

#### RESULT 1

US-09-236-080-5  
; Sequence 5, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236, 080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1994  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-236-080-5

Alignment Scores:  
Pred. No.: 9.67e-237 Length: 1994  
Score: 1870.00 Matches: 368  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.31% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x US-09-236-080-5 (1-1994)

QY	1	MetAlaLaProAspLeuLeuAspProLysSerAlaGlnAsnSerLysProArgLeu	20
Db	484	ATGGCGGCCCTGACTTGTGGATCCAAAGTCTGTGCTCAGAACTCCAAACCGAGGCTC	543
QY	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	544	TCATTCTCTTCAAAACCCACCGGTGCTTGTCTCCCGGGTGGAGAGTACTCGGCATTAA	603



GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: NO. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1246  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-236-080-1

Alignment Scores: 3,47e-232 Length: 1246  
Pred. No.: 1833.00 Matches: 356  
Score: 98.91% Conservativeness: 8  
Percent Similarity: 96.74% Mismatches: 4  
Best Local Similarity: 97.34% Indels: 0  
Query Match: 3 Gaps: 0  
DB:

US-09-655-272-4 (1-370) x US-09-236-080-1 (1-1246)

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QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
DB 664 GAGGCCCGGTGTTCAAGCAATGGAGCAGCTCAGGAGATTTCAGAGGACCAACCAAT 723  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 724 GTGATCCAGAGCAGACCTTCATAGCCAGCATGTAGCCAGCATGTGCTCACTCCACGAGCTGAC 783  
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 784 GAACCTATCCAGCAATAGTGGCAGCAATATACCGCAGGATTTATCCCTTAGGAACACAGC 843  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 844 TCCAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTCTTGGTGGTACTGTTATC 903  
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
DB 904 ACACCATAGGATTGGAAACATCTCCACGACACTGAAGTGGAAATATATTCGATC 963  
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
DB 964 ATCTATGCTTGTGGGAATTCCTCTTGGCTTCTACTGGCTGGGGTGGTGGATCAG 1023  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
DB 1024 CTAGGAACATATTTGGAAAGGAATTCGCAAGAGTGGAGACACATATTTAATGATGAAAT 1083  
QY 201 ValSerGlnThrLysIleArgIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
DB 1084 GTTAGTCAGACGAGATTCGTATCATCTCCACCATCATCTTCTCTTGGTGGTCTGTC 1143  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
DB 1144 CTCTTGTGGCTCTCCCTCGCGGTATATTCAGGACATAGAGGCTGGAGCGGCTGGAC 1203  
QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
DB 1204 GCTATCTATTTGTGGTATCATCTGACGACCATTCGATTTGGAGACTACGTGGCAGGT 1263  
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
DB 1264 GGATCAGACATTAATCTGACATCTTACAGGCTGTGGTGGTGGTCTGATCTCT 1323  
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
DB 1324 GGGCTGGCTACTTTGGAGCTGTTCTGAGCATGATTGGGACTGGCTACGGGTGATCTCT 1383  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
DB 1384 AGAAGACCGAGAGAGAGTGGAGAGTTTCAGAGCGCATGCGCTGAGTGACAGCCAAAT 1443  
QY 321 ValThrAlaGluPheLysGlnThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
DB 1444 GTCACGCCCGAGTTCAAGAAACAGAGGCGGCTGAGCGTGAGATCTACGACAAAGTTC 1503  
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1504 CACGTGGCCACATCCGTGAGCGGAAGCTCTCGCAGAGCTGGCGGCAACCAACCAAG 1563  
QY 361 GluLeuThrProCysMetArgThr 368  
DB 1564 GAACCTGACTCCGTGATGAGGACC 1587

RESULT 2  
US-09-236-080-1  
; Sequence 1, Application US/09236080  
; Patent No. 6242217



Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
Db 729 GCCATTTATTTGTGGTTATCACTAAACAACTATTGGATTGGTGAAGTTCAGGT 788  
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
Db 789 GGATCCGATATTGAATATCTGGACTCTTAAGCCTGTGTGGTTCTGGATCCCTTGTA 848  
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 849 GGGCTTGCTTACTTGTCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 908  
Qy 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
Db 909 AAAAAGACAAAGAGAGGTTGGAGAGTTTCAGAGCACACGCTGCTGAGTGAGACCAAC 968  
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
Db 969 GTACAGCCGAAATTCAGAAACAGAGGCGGACTGAGTGTGGAGATTATGACAAAGTTC 1028  
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1029 CAGCGGCCACCTCCATCAAGCGGAAGCTCTCGCGAAGACTGGCTGGAAACCAATCAG 1088  
Qy 361 GluLeuThrProCysMetArgThr 368  
Db 1089 GAGCTGACTCCTTGTAGGAGACC 1112

## RESULT 3

US-09-336-643A-82  
; Sequence 82, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 3300  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50)...(1285)  
US-09-336-643A-82

Alignment Scores:  
Pred. No.: 1,76e-231 Length: 3300  
Score: 1833.00 Matches: 356  
Percent Similarity: 98.91% Conservative: 8  
Best Local Similarity: 96.74% Mismatches: 4  
Query Match: 97.34% Indels: 0  
DB: 3 Gaps: 0

US-09-655-272-4 (1-370) x US-09-336-643A-82 (1-3300)

Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
Db 50 ATGGCGGCACCTGACTTGTGGATCTTAATCTGCCGCTCAGAACTCCAAACCGAGCTC 109

Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
Db 110 TCGTTTTCACGAAACCCACAGTGTCTCCCGGTGGAGAGTGCACGACCAATTAAT 169  
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
Db 170 GTTATGAATGGAAGACGGTCTCCAGATATTCCTGGTGTGTCTCTATCTGATCATC 229  
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80  
Db 230 GGAGCCACCGTGTTCAAAGCATTTGGAGACGCTCATGAGATTTTCACAGAGACCACT 289  
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
Db 290 GTGATCCAGAAGCAAAACATTCATATCCCAACATTCCTGTCTCAATTCGACGAGCTGGAT 349  
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
Db 350 GAATCATTCAGCAATATAGTGGCAGCANTAATGCAGGGATATATACGTTAGGAACACC 409  
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
Db 410 TCCATCAATCAGTCAGTGGGATTTGGGAAGTTCCTCTCTTCTGCTGGCACTGTTATT 469  
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
Db 470 ACAACCATAGGATTTGGAAACATCTCACACGCACAGAAAGCGCGCAAAATATTCTGTATC 529  
Qy 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsnGln 180  
Db 530 ATCTATGCTCTTACTGGGAATCCCTCTTGTGTTTCTCTTGGCTGGAGTTGGAGATCAG 589  
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
Db 590 CTAGGCACCATATTTGGAAGAAATGCAAGTGGAGATACGTTTATTAAGTGAAT 649  
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
Db 650 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATATCTATTGGCTGTGTA 709  
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
Db 710 CTCTTTGTGGCTCTGCTCGCATATATTCAACACATAGAGCGTGGAGTGCCTGGAC 769  
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
Db 770 GCCATTTATTTGTGGTTATCACTTAACAACATATTGGATTGGTGTGCTGACGTTCAGGT 829  
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
Db 830 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTGCTGTGTCTGGATCCCTGTA 889  
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 890 GGGCTTGTCTTACTTGTCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT 949  
Qy 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
Db 950 AAAAGACAAAGAGAGGTTGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCAAC 1009  
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
Db 1010 GTCACAGCGCAATTCAAAGAAACCCAGAGGCGCACTGAGTGTGGAGATTATGACAAAGTTC 1069  
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1070 CAGCGGCCACCTCCATCAAGCGGAAGCTCTCGCGAAGACTGGCTGGAAACCAATCAG 1129  
Qy 361 GluLeuThrProCysMetArgThr 368  
Db 1130 GAGCTGACTCCTTGTAGGAGGACC 1153

RESULT 4

[illegible]

```

US-09-799-451-432
; Sequence 432, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 432
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS (2086)
; LOCATION: (473)..(2086)
US-09-799-451-432

Alignment Scores:
Score: 3.73e-154 Length: 2730
Pred. No.: 1247.50 Matches: 247
Percent Similarity: 78.07% Conservative: 52
Best Local Similarity: 64.49% Mismatches: 67
Query Match: 66.25% Indels: 17
DB: 4 Gaps: 5

US-09-655-272-4 (1-370) x US-09-799-451-432 (1-2730)
Qy 2 AlaalaProAspLeuAspProLySerAla-----Ala 13
Db 521 GCACGACGACCGGTGTCCACGCCACAGAGCGCCACTAACGGGCAACCCCGGCTCCGGCT 580
Qy 14 GlnAsnSerLySProArgLeuSerPheSerSerLySProThrValLeuAlaSerArgVal 33
Db 581 CCGACTCCAACTCCGCGCGCTGTCCATTCTCTCCGAGCCACACGTGTAGCC---AGGATG 637
Qy 34 GluSerAspSer-----AlaAlaAsnValMetLySTrpLySThrValSerThrIle 50
Db 638 GAAGGACCTCCCAAGGGGGGTTCCACACCGTCAATGAAGTGAAGACGGTGTGGCATC 697
Qy 51 PheLeuValValValLeuLySLeuIleIleGlyAlaAlaValPheLySAlaLeuGluGln 70
Db 698 TTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 757
Qy 71 ProGlnGluIleSerGlnArgThrThrIleValIleGlnLySglnThrPheIleAlaGln 90
Db 758 CCCTTTGAGAGCAGCAGCAGATACCATCCCTCTGGAGAGGCGGAATTCCTCGCGGAT 817
Qy 91 HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaAlaIle 110
Db 818 CATGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 877

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; LENGTH: 1182
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-1

Alignment Scores:
Pred. No.: 3,69e-95 Length: 1182
Score: 797.00 Matches: 145
Percent Similarity: 72.18% Conservative: 60
Best Local Similarity: 51.06% Mismatches: 77
Query Match: 42.33% Indels: 2
DB: 4 Gaps: 1

US-09-655-272-4 (1-370) x US-09-432-470-1 (1-1182)
QY 42 MetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuValLeuValGly 61
DB 1 ATGGCGCAGCACCGCTCTGGCCCTGCTGGCGCTGCTGCTTACTTGTGTCTGTGT 60
QY 62 AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIleVal 81
DB 61 GCCTGTGTTCGGGCGCTTGGAGCAGCCCGCCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101
DB 121 GAGGTCCGAGAGAAAGTTCTGAGGGCCCATCTGCTGTGAGCGACCCAGAGCTGGGCTC 180
QY 102 LeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121
DB 181 CTATCAAGAGGTGCTGATGCTGCTGGGAGGGGCTGGGAGCCAGAACCACTCGACC 240
QY 122 AsnGlnValSerHis-----TrpAspLeuGlySerSerPhePheAlaGlyThrVal 139
DB 241 AGCAACAGAGCCACCTCAGCTCGGACCTGGGAGCGGCTCTCTTTCTCAGGGAGCATC 300
QY 140 IleThrThrIleGlyPheGlyAsnIleSerProArgThrCluGlyLysIlePheCys 159
DB 301 ATCACCACCATCGCTATGCAATGCGCCCTGCGGACGATCCCGGGCGGCTCTTCTGTC 360
QY 160 IleIleValAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179
DB 361 ATCTTTATGCGTGTGGGATTCGCTGTTGGGATCTCTATCGGAGGGGTCTGGGAC 420
QY 180 GlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrp 199
DB 421 CGGCTGGGCTCTCTCCCTCGCCCATGCGATCGGTACATTCGATTCGAGAGTGG 480
QY 200 AsnValSerGlnThrLysIleArgIleIleSerThrIleIlePheIlePheGlyCys 219
DB 481 CAGTGTCCACCGGAGGTAGTAAGAGTGTGTGCGGATGCTTTTCTGCTGATCGGCTGC 540
QY 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeu 239
DB 541 CTGCTCTTGTCTCAGCCCGCATGCTGCTGCTATATGAGGACTGGAGCAAGCTG 600
QY 240 AspAlaIleTrpPheValValIleThrLeuThrIleGlyPheGlyAspTrpValAla 259
DB 601 GAGGCCATCTACTTGTCTATGATGACGCTTACCACCGTGGGCTTGGCGACTATGTTGCC 660
QY 260 GlyCysSerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeu 279
DB 661 GCGCGGAGACCCAGGAGGACTCCCGGCGCTATCAGCCGCTGTGTGTGTGTGTGTGTGT 720
QY 280 ValCysLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIle 299
DB 721 CTGCGCTGCTTACTTCTGCTCAGTGCTCAGCACCATCGGGAACCTGGCTGCGAGTAGTG 780
QY 300 SerLysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAla 319
DB 781 TCCCGCGCACTCGGCGAGAGATGGGCGGCTCAGCGCTCAGGCTGCGAGCTGCACTGGC 840
QY 320 AsnValThrAla 323
DB 320 AsnValThrAla 323
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DB 841 ACAGTGACAGCG 852

RESULT 6
US-09-432-470-3
; Sequence 3, Application US/09432470
; Patent No. 6436197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-3

Alignment Scores:
Pred. No.: 3,88e-95 Length: 1218
Score: 797.00 Matches: 145
Percent Similarity: 72.18% Conservative: 60
Best Local Similarity: 51.06% Mismatches: 77
Query Match: 42.33% Indels: 2
DB: 4 Gaps: 1

US-09-655-272-4 (1-370) x US-09-432-470-3 (1-1218)
QY 42 MetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuValIleGly 61
DB 37 ATGGCGCAGCACCGCTCTGGCCCTGCTGGCGCTGCTGCTTACTTGTGTCTGTGT 96
QY 62 AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIleVal 81
DB 97 GCCTGTGTTCGGGCGCTTGGAGCAGCCCGCCAGCAGCAGCAGCAGCAGCAGCAGCAG 156
QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101
DB 157 GAGGTCCGAGAGAAAGTTCTGAGGGGCCCATCTCGTGTGTGAGCCAGCAGGAGCTGG 216
QY 102 LeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121
DB 217 CTATCAAGAGGTGCTGATGCCCTGGGAGGGGTGGGACCCAGAACCACTCGACC 276
QY 122 AsnGlnValSerHis-----TrpAspLeuGlySerSerPhePheAlaGlyThrVal 139
DB 277 AGCAACAGAGCCACCTCAGCTGGGACCTGGGAGCGGCTCTTTTCTCAGGAGCATC 336
QY 140 IleThrThrIleGlyPheGlyAsnIleSerProArgThrCluGlyLysIlePheCys 159
DB 337 ATCACCACCATCGGCTATGCAATGCGCCCTGCGCAGACAGATCCCGGGCGGCTCTTCTGC 396
QY 160 IleIleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179
DB 397 ATCTTTATGCGTGTGTGGGATTCGCTGTTGGGATCTCTATGCGAGGGGTGGGAC 456
QY 180 GlnLeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrp 199
DB 457 CGGCTGGGCTCTCCCTCGGCCATGCGATCGGTACATTCGATTCGAGAGTGG 516
QY 200 AsnValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCys 219
DB 517 CAGCTGCCACCGAGGTAGTAAGAGTGTGTGCGGATGCTTTTCTGCTGATCGGCTGC 576
QY 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeu 239
DB 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeu 239
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Db 370 CCCAACGATGGTCCCGCTCTTCTGATCTCTTTGCCCTTGGGGATCCCACTC 429
Qy 170 PheGlyLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIle 189
Db 430 AACCTCGTGGTCTC-----AACCGACTGGGCGATCTCATGACGAGGAGTA 477
Qy 190 -----AlaLysValGluAspThrPheIleLysTrpAsnValSerGlnThrLys 205
Db 478 AACCACTGGGCGAGCGCTGGGGGCACT-----TGGCAG---GATCCTGACAAG 525
Qy 206 IleArgIleLeuSerThrIlePheLeuPheGlyCysValLeuPheValAlaLeu 225
Db 526 GCGCGGTGGCTGGCGGCTCTGGCGCTCTCTCTGGGCTCTCTCTCTCTCTCTCT 585
Qy 226 ProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheVal 245
Db 586 CCACCGTGTCTCTCCACATGAGGCTGGAGCTACACAGAGGCTTCTACTTCGCC 645
Qy 246 ValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGlyLysSerAspIleGlu 265
Db 646 TTCATCACCTCAGCACCGTGGGCTTCGCGACTACGTGATTGGAATGAACCCCTCCAG 705
Qy 266 ---TyrLeuAspPheTyrLysProValValTyrPheThrIleLeuValGlyLeuAlaTyr 284
Db 706 AGGTACCACTGGTGTACAAGACATGGTGTCCCTGTGGATCTCTTTTGGGATGGCATGG 765
Qy 285 PheAlaAlaValLeuSerMetIle 292
Db 766 CTGGCTTGTATCAAACTCATC 789
```

## RESULT 15

```
US-09-431-367B-6
; Sequence 6, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
US-09-431-367B-6
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Alignment Scores:
Pred. No.: 4.86e-41 Length: 996
Score: 387.00 Matches: 88
Percent Similarity: 56.05% Conservative: 51
Best Local Similarity: 35.48% Mismatches: 95
Query Match: 20.55% Indels: 14
DB: 4 Gaps: 6
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US-09-655-272-4 (1-370) x US-09-431-367B-6 (1-996)

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Qy 50 IlePheLeuValValLeuTyrLeuIleGlyAlaAlaValPheLysAlaLeuGlu 69
Db 73 CTGCTGCTCGCTACCTGGCTTACCTGGCGCTGGGACCGCGCTGTCTGGACGCTGGAG 132
Qy 70 GlnProGlnGluIleSerGlnArgThrIleValIleGlnLysGlnThrPheIleAla 89
Db 133 GGCGCGCGCGCGGAGGACTCCAGCGCAGCTTCCAGCGGACAAAGTGGGAGCTGTTCAG 192
Qy 90 GlnHieAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaAla 109
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Db 193 AACTTCACGTGTGAGCCGCCCGCTGGACTCGCTGATCCGGGATGTCTGTCGAAGCA 252
Qy 110 IleAsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeu 129
Db 253 TACAAAAACGAGCCAGCCCTCTCTCAGACACACACACAGC---ATGGGGCGCTGGGAGCTC 309
Qy 130 GlySerSerPhePhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSer 149
Db 310 GTGGGCTCCTCTCTCTTTCTGTGTCCACCATCACCACCATTTGGCTATGCAACCTCAGC 369
Qy 150 ProArgThrGluGlyCysIlePheCysIleIleTyrAlaLeuLeuGlyIleProLeu 169
Db 370 CCCAACACATGGCTGGCGCTCTCTGATCTCTTTGGCCCTTGTGGGATCCCACTC 429
Qy 170 PheGlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIle 189
Db 430 AACCTCGTGGTCTC-----AACCGACTGGGCGATCTCATGACGAGGAGTA 477
Qy 190 -----AlaLysValGluAspThrPheIleLysTrpAsnValSerGlnThrLys 205
Db 478 AACCACTGGGCGAGCGCTGGGGGCACT-----TGGCAG---GATCCTGACAAG 525
Qy 206 IleArgIleLeuSerThrIlePheIleLeuPheGlyCysValLeuPheValAlaLeu 225
Db 526 GCGCGGTGGCTGGCGGCTCTGGCGCTCTCTCTGGGCTCTCTCTCTCTCTCTCTCT 585
Qy 226 ProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheVal 245
Db 586 CCACCGCTGTCTTCTCCACATGAGGCTGGAGCTACACAGAGGCTTCTACTTCGCC 645
Qy 246 ValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGlyLysSerAspIleGlu 265
Db 646 TTCATCACCTCAGCACCGTGGGCTTCGCGACTACGTGATTGGAATGAACCCCTCCAG 705
Qy 266 ---TyrLeuAspPheTyrLysProValValTyrPheThrIleLeuValGlyLeuAlaTyr 284
Db 706 AGGTACCACTGGTGTACAAGACATGGTGTCCCTGTGGATCTCTTTTGGGATGGCATGG 765
Qy 285 PheAlaAlaValLeuSerMetIle 292
Db 766 CTGGCTTGTATCAAACTCATC 789
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Job time : 109.727 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 3, 2005, 01:34:36 ; Search time 648.464 Seconds  
(without alignments)  
3278.486 Million cell updates/sec

Title: US-09-655-272-4

Perfect score: 1883

Sequence: 1 MAAPDLLDPKSAQAQKPRLL.....SABLGNHNOELTPCMTCL 370

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastp -SUFFIX=rbp -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=biosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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Database :

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1827	97.0	2391	18	US-10-349-528-9
5	1805	95.9	2130	8	US-08-816-011-46
6	1247.5	66.3	1614	11	US-09-892-360-1
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10	1247.5	66.3	2065	9	US-09-729-920-1
11	1247.5	66.3	2065	18	US-10-887-932-1
12	1247.5	66.3	2730	16	US-10-302-172-432
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32	572.5	30.4	1265	16	US-10-276-774-1249
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# ALIGNMENTS

RESULT 1  
US-09-828-746-5  
; Sequence 5, Application US/09828746  
; Patent No. US2002028485A1  
; GENERAL INFORMATION:  
; APPLICANT: Helen Jane Meadows  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30031-D1  
; CURRENT APPLICATION NUMBER: US/09/828,746  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 09/236,080  
; PRIOR FILING DATE: 1999-01-25  
; PRIOR APPLICATION NUMBER: EP 98300570.3  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: UK 9822135.1  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1994

; TYPE: DNA			
; ORGANISM: HOMO SAPIENS			
US-09-828-746-5			
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Score:	1870.00	Matches:	368
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.31%	Indels:	0
DB:	9	Gaps:	0
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Qy	21	SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	544	TCATTCCTTCAAAACCCCGCTGCTTCCCGGTGGAGTACTCGGCATTAAAT	603
Qy	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTyrLeuIleIle	60
Db	604	GTATGAATGGAAGACAGCTCCACGATTTCTCGTGTGCTCTACCTGATCATC	663
Qy	61	GlyAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle	80
Db	664	GGAGCGCGGTGTTCAAAGGATTTGGAGCGCTCAGAGATTTCCCGAGGACCACT	723
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
Db	724	GTGATCCAGAGCAGACCTTCATAGCCAGCATGCTCGCTCACTCCACCGAGCTGGAC	783
Qy	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
Db	784	GAATCATCCAGCAAAATAGTGGCAGCAATTAACGAGGATTTATCCCTTTAGGAAACAGC	843
Qy	121	SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140
Db	844	TCCAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTTCTTGTGCTACTGTATC	903
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160
Db	904	ACAACCATAGATTTGGAAACATCTCCACCAAGTGAAGTGGAAATATTTCTGCATC	963
Qy	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln	180
Db	964	ATCTATGCTTGTGCGGAATTCCTCTTTGGCTTTCTTACTGGCTGGGTGGTATCAG	1023
Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	1024	CTAGGAATATATTTGGAAAGGAATTCGAAGATGGGAAGACACATTTATTAAGTGGAT	1083
Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	1084	GTATCTCAGACGAATTCGATCATCTCCACCATCTTTCATCTTGTGCTGTGTC	1143
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	1144	CTCTTTGTGCTCTCCCTCGCGTCATATTCAGCAATAGAGGCTGGAGCGCCCTGGAC	1203
Qy	241	AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly	260
Db	1204	GCTATCTATTTGTGGTTATCTCTGACGACCATTTGGATTTGGAGACTAGCTGGCAGGT	1263
Qy	261	GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal	280
Db	1264	GGATCAGACATTGAATATCTGACATCTTACAAGCCTGTGTGTGTTCTGGATCTCTGTT	1323
Qy	281	GlyLeuAlaTyrPheAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
Db	1324	GGGCTGGCCTACTTTTGCAGCTGTCTTGACATGATTTGGGACTGGCTGAGGTGATCTCT	1383

Qy	301	LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320
Db	1384	AGAAGACGAAGGAAGAGTGGGAGAGTTTCAGAGCGCATCGCGTGGACAGCCAAT	1443
Qy	321	ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe	340
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Qy	341	GlnArgAlaThrSerValLysArgLysSerAlaGluLeuAlaGlyAsnHisAsnGln	360
Db	1504	CAGCGTCCCATCATCGTGAAGCGGAAGCTCTCCGAGAGCTGGCGGCAACCAACACAG	1563
Qy	361	GluLeuThrProCysMetArgThr	368
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RESULT 2

US-09-828-746-1

; Sequence 1, Application US/09828746

; Patent No. US2002028485A1

; GENERAL INFORMATION:

; APPLICANT: Helen Jane Meadows

; APPLICANT: Conrad Gerald Chapman

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30031-D1

; CURRENT APPLICATION NUMBER: US/09/828,746

; PRIOR FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: US 09/236,080

; PRIOR FILING DATE: 1999-01-25

; PRIOR APPLICATION NUMBER: EP 98300570.3

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: UK 9822135.1

; PRIOR FILING DATE: 1998-10-09

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1246

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

US-09-828-746-1

Alignment Scores:

Pred. No.: 5.45e-189

Length: 1246

Score: 1833.00

Matches: 356

Percent Similarity: 98.91%

Conservative: 8

Best Local Similarity: 96.74%

Mismatches: 4

Query Match: 97.34%

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DB: 9

Gaps: 0

US-09-655-272-4 (1-370) x US-09-828-746-1 (1-1246)

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Qy	21	SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
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Qy	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTyrLeuIleIle	60
Db	129	GTATGAATGGAAGACGGTCTCCAGCATTTCTCGTGTGTTGCTCTCTATCTGATCATC	188
Qy	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle	80
Db	189	GGAGCCACCGTGTTCAAAGCATTTGGAGCGCTCATGAGATTTTCAGAGGACCACTT	248
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
Db	249	GTGATCCAGAAGCAAACTTCATATCCCAACATCTCTGTGTCTTGTGCTGCGAGCTGGAT	308
Qy	101	GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120

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Db 309 GAACATTCAGCAATAGTGGCAGCAATAAATGACGGATTATACCGTTAGAAACACC 368
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Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
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Qy 201 ValSerGlnThrIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
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Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
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Qy 241 AlaIleTrpPheValValIleThrLeuThrThrIleGlyPheGlyAspTrpValAlaGly 260
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Db 849 GGGCTTGCTTACTTGTCTGCTGCTGAGCATGATTGGAGATTGGCTCGAGTGATATCT 908
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
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Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTrpAspLysPhe 340
Db 969 GTACAGCCGATTCAAAGAAACAGAGGCGACTGAGTGTGAGATTATGACAAAGTTC 1028
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1029 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAGAACTCGCTGGAAACCAATATCAG 1088
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1089 GAGCTGACTCTCTGTAGGAGACC 1112

RESULT 3
US-10-121-746-82
; Sequence 82, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)....(1285)
US-10-121-746-82

Alignment Scores:
Pred. No.: 2,22e-188 Length: 3300
Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservative: 8
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 14 Gaps: 0

US-09-655-272-4 (1-370) x US-10-121-746-82 (1-3300)
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Db 50 ATGGCGGCACCTGACTTGTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 109
Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 110 TCGTTTTCACAAACCCACAGTGTCTTCCGGGTGGAGTGACAGCACCATTAAT 169
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTrpIleLeuIle 60
Db 170 GTTATGAATGGAAGCGGTCTCCAGATATCTTGGTGTGTCTCTATCTGATCATC 229
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80
Db 230 GGAGCCACCGTGTCAAAGCATTTGGAGCAGCCTCATGAGATTTTCACAGAGGACCACCAT 289
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 290 GTGATCCAGAAACCAACATTCATATCCCAACATTTCTGTGTCATTCGACGGAGCTGGAT 349
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 350 GAACCTCATTCACCAATAGTGGCAGCAATAATGAGGGATTATACCGTTAGGAACACC 409
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 410 TCCAAATCAATCAGTCACCTGGGATTGGGAAGTTCCTTCTTCTTGTGCTGCACTGTTATT 469
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160
Db 470 ACAACCATAGGATTGGAAACATCTCACACGCACAGAAAGGGCGCAAAATATCTGTATC 529
Qy 161 IleTrpAlaLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
Db 530 ATCTATGCTTACTGGGAATTCCTCTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 589
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 590 CTAGGCACCATATTTGGAAAGGAATTTGCCAAAGTGAAGATACGTTTATTAAGTGAAT 649
Qy 201 ValSerGlnThrIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 650 GTTAGTCAGACCAAGATTGGCATCATCTCAACAATCATATTTATATCTATTTGGCTGTGA 709
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 710 CTCCTTGTGGCTCTGCTCGATCATATTCAAACACATAGAGGCTGGAGTGGCCCTGGAC 769
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QY 241 AlalleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
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 Db 1010 GTCACAGCCGAATTCAAAGAAACACAGAGGCGACTGAGTGTGAGATTTATGACAAAGTTC 1069  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 Db 1070 CAGGGGCCACCTCCATCAAGCGAGGCTTCGGCAGAACTGGCTGGAACACCAATCAG 1129  
 QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1130 GAGCTGACTCTTGTAGGAGGACC 1153  
 RESULT 4  
 US-10-349-528-9  
 ; Sequence 9, Application US/10349528  
 ; Publication No. US2004025368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RAMANATHAN, Chandra  
 ; APPLICANT: GOPAL, Shuba  
 ; APPLICANT: MINIER, Gabe  
 ; APPLICANT: FEDER, John  
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF  
 ; FILE REFERENCE: D0210  
 ; CURRENT APPLICATION NUMBER: US/10/349,528  
 ; CURRENT FILING DATE: 2003-01-22  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO 9  
 ; LENGTH: 2391  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-10-349-528-9  
 Alignment Scores: Length: 2391  
 Pred. No.: 6,27e-188 Matches: 254  
 Score: 1827.00  
 Percent Similarity: 98.91% Conservative: 10  
 Best Local Similarity: 96.20% Mismatches: 4  
 Query Match: 97.03% Indels: 0  
 DB: 18 Gaps: 0  
 US-09-655-272-4 (1-370) x US-10-349-528-9 (1-2391)  
 QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnSerLysProArgLeu 20  
 Db 586 TTGGCGGCACCTGACTTGTGTTGATCTCTAAATCTGCGCTCAGAACTCCAAACCCGAGGCTC 645  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 Db 646 TCGTTTTCACAAACCCACAGTGTCTTCCCGGTGGAGGTGACACGACCACTAAT 705  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLysLeuIle 60  
 Db 706 GTTATGAATGAAGACAGGCTCCACCATATCTGTTGTTGTTCTCTATCTGATCATC 765  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnLysLeuSerGlnArgThrThrIle 80

Db 766 GGAGCCACCGTGTTCARAGCATTTGGAGCAGCTCATGAGATTTTCACAGAGACCACCAT 825  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 826 GTGATCCAGAGCAACCAATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 885  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 886 GAACTCATTCAGCAATAGTAGGCACCAATAAATGCAGGATATATACCGTTAGGAACAC 945  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 Db 946 TCCAAATCAATCAGTCAGTGGGATTTGGGAAGTTCCTCTCTTTTCTGCTGGCACTGTTAT 1005  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 1006 ACAACCATAGGATTTGGAAACCAATCTCACCCGACACAGAGGCGCAAAATATTTCTGTATC 1065  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 1066 ATCTATGCTTACTGCGAATTTCCCTCTTTTGTCTTCTTGTGCTGGAGTTGGAGATCAG 1125  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 1126 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAAAGATACGTTTATTAACTGGAAT 1185  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 1186 GTTAGTCAGACCAAGATTCGCATCATCTCAACATCATATTTATATTTGCTGTGTA 1245  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 1246 CTCTTTGTGGCTCTGCTGCGATCATATTCAAACATAGAGGCTGGAGTGCCTGGAC 1305  
 QY 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260  
 Db 1306 GCCATTATTTTGTGTTTATCACTTAACTATTTGGTGGTACTACGTTGAGGT 1365  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrrPheTrrPheIleVal 280  
 Db 1366 GGATCCGATATTGAATATCTGAGCTTCTTAAGCTCTGCTGTGTTCTGATCTGATATCT 1425  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrrPheValIleSer 300  
 Db 1426 GGGCTTGTCTTACTTGTCTGCTGCTGAGCATGATTTGGAGATTTGGCTCCGAGTGTATCT 1485  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrrPheAlaAsn 320  
 Db 1486 AAAAGACAAAGAGGTGGAGGTTCAAGACACACGCTGCTGAGTGGACAGCCCAAC 1545  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe 340  
 Db 1546 GTCACAGCGCAATTCAGAAACACAGAGGCGGCTGAGTGTGGAGATTTATGACAAGTTC 1605  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 Db 1606 CAGCGGCGCACCTCCATCAAGCGGAAGCTCTCGGAGAACTCGGCTGGAAACCAACATCAG 1665  
 QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1666 GAGCTGACTCTTGTAGGAGGACC 1689  
 RESULT 5  
 US-08-816-011-46  
 ; Sequence 46, Application US/08816011  
 ; Publication No. US20030165806A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Price, Laura A.  
 ; APPLICANT: Pausch, Mark H.  
 ; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences  
 ; TITLE OF INVENTION: Encoding Them, and Methods of Using Same  
 ; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: American Home Products Corporation  
 ; STREET: One Campus Drive  
 ; CITY: Parsippany  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07054  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/816,011  
 ; FILING DATE: 11-MAR-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Matthews, Gale F.  
 ; REGISTRATION NUMBER: 32,269  
 ; REFERENCE/DOCKET NUMBER: 32,421-C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-683-2134  
 ; TELEFAX: 201-683-4117  
 ; INFORMATION FOR SEQ ID NO: 46:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2130 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-816-011-46

## Alignment Scores:

Pred. No.: 1.3e-185 Length: 2130  
 Score: 1805.00 Matches: 352  
 Percent Similarity: 98.37% Conservative: 10  
 Best Local Similarity: 95.65% Mismatches: 6  
 Query Match: 95.86% Indels: 0  
 DB: 8 Gaps: 0

US-09-655-272-4 (1-370) x US-08-816-011-46 (1-2130)

QY 1 MetAlaAlaProAspLeuLeuAppProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 223 GTGGCGGCGACCTGACTGTGTGGATCTCAATCTGCGCTCAGAACTCCAAACCGAGGCTC 282  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 DB 283 TCATTTTCCAGAAACCCACAGTGTCTTCCGGGTGGAGTGCACGACCATTAAT 342  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuThrLeuIleIle 60  
 DB 343 GTTATGAATGGAAGACGGTCTCCAGATATCTCGTGTGTCTCTATCTGATCATC 402  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 DB 403 GGAGCACCGTGTTCAAAGCATTTGGAGCAGCCTCATGAGATTTTCAGAGGACCCATT 462  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 463 GTGATCCAGAGCAACATTCATATCCCAACATCTCTGTCTCAATTCGACGGAGCTGGAT 522  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 DB 523 GAACTCATTCAGCAATAGTGGCAGCAATAATGCGAGGATTATACCGTTAGGAACACC 582  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 DB 583 TCCAATCAATCAGTCACTGGGATTTGGGAAGTTCCTTCTCTTCTGCGACTGTATT 642  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160  
 DB 643 ACAACCATAGGATTTGGAAACATCTCACCACGCACAGAGGCGGCAAAATATTTCTGTATC 702

QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 DB 703 ATCTATGCTTATCGGAATTCCTCTTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 762  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 DB 763 CTAGGCACCATATTTGGAAAGGAATTGCCAAGTGAAGATACGTTTATTAGTGAAT 822  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIlePheIleLeuPheGlyCysVal 220  
 DB 823 GTTAGTCAGACCAAGATTCGCATCTCTCAACAATCATATTTATCTATTTGGCTGTGTA 882  
 QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
 DB 883 CTCCTTTGTGGCTCTGCTCGCATCATATTCAAAACACATAGAAGCTGGAGTGCCTGGAC 942  
 QY 241 AlaIleTyrPheValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260  
 DB 943 GCAATTTATTTTGGTTATCACTCTAACACTATTGGATTGGTGTACTACGTTGAGGT 1002  
 QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280  
 DB 1003 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGCTGTGTGTCTTGGATCTTGTGA 1062  
 QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
 DB 1063 GGGCTTTGCTTACTTTGCTGCTCTGTCGATGATTTGGGAGATTTGGCGAGTATCT 1122  
 QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 DB 1123 AAAAGACAAAGAGAGGTGGAGATTTCAGAGCACGCTGCTGAGTGGAGCGCAAC 1182  
 QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340  
 DB 1183 GTCACAGCCGATTCAAAGAACAGGAGCGACTGAGTGTGGAGATTTATGACAGTTC 1242  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
 DB 1243 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGAGAACTCGCTGGAACCAATCAG 1302  
 QY 361 GluLeuThrProCysMetArgThr 368  
 DB 1303 GAGCTGACTCTTGTAGGAGGACC 1326

## RESULT 6

; US-09-892-360-1  
 ; Sequence 1, Application US/09892360  
 ; Publication No. US20040101833A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LAZDUNSKI, MICHEL  
 ; APPLICANT: LESAGE, FLORIAN  
 ; APPLICANT: ROMEO, GEORGES  
 ; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE  
 ; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
 ; FILE OF INVENTION: RILUZOLE  
 ; FILE REFERENCE: 1256-R-00  
 ; CURRENT APPLICATION NUMBER: US/09/892,360  
 ; PRIOR FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: 60/214,559  
 ; PRIOR FILING DATE: 2000-06-27  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1614  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1614)  
 ; OTHER INFORMATION: ORF of human TREK2 cDNA  
 ; US-09-892-360-1

Alignment Scores:

Pred. No.:	3 37e-125	Length:	1614
Score:	1247.50	Matches:	247
Percent Similarity:	78.07%	Conservative:	52
Best Local Similarity:	64.49%	Mismatches:	67
Query Match:	66.25%	Indels:	17
DB:	11	Gaps:	5

US-09-655-272-4 (1-370) x US-09-892-360-1 (1-1614)

Qy	2	AlaAlaProAspLeuLeuAspProLysSerAla-----Ala 13
Db	49	GCAGCAGCACCCTCCCAAGGGGCTTGCAGACCGTCATGAAGTGAAGACGGTGTTCCTCC
Qy	14	GlnAsnSerLysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33
Db	109	CCGACTCCAACTCGGCGCTTGCTTCCTCCGAGCCACAGTGTAGCC---AGGATG 165
Qy	34	GlusSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrile 50
Db	166	GAAGGCACCTCCCAAGGGGCTTGCAGACCGTCATGAAGTGAAGACGGTGTTCCTCC
Qy	51	PheLeuValValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 70
Db	226	TTTGT
Qy	71	ProGlnGluLysSerGlnArgThrThrileValIleGlnLysGlnThrPheIleAlaGln 90
Db	286	CCCTTTGAGACGACCCAGAGAGATACCATCGCTTGGAGAAGCGGAATTCCTCGGGAT 345
Qy	91	HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaAlaIle 110
Db	346	CATGCTGT
Qy	111	AsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130
Db	406	AATGGGGAGTCAGTCCCAATAGGAATCTTCCCAACACAGACGACCACTGGGACCTCGGC 465
Qy	131	SerSerPhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerPro 150
Db	466	AGTGCTTTTCTTTCTGT
Qy	151	ArgThrGluGlyGlyLysIlePheCysIleIleIleValAlaLeuLeuGlyIleProLeuPhe 170
Db	526	ACGACTGAGAGGAGGCAATCTTTGTATTTATATGCACTCTTGGAAATCCACTCTTT 585
Qy	171	GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190
Db	586	GGTTTCTTATTGGCTGGAATTTGGAGCAACACTTGGAACTCTTTGGAAATCCACTCTTT 645
Qy	191	LysValGluAspThrPheIleLysTrpAsnValSerGlnThrLysIleArgIleIleSer 210
Db	646	AGAGTGGAGAGGCTTTTCGAAAAAAGACGATGAGTCAGACCAAGATCCGGGTCTATCTCA 705
Qy	211	ThrIleIlePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230
Db	706	ACCATCTGTTCATCTTGGCGGCTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy	231	LysHisIleGluGlyTrpSerAlaLeuAspAlaIleTyPheValValIleThrLeuThr 250
Db	766	AAGTACATCGAGGCTTGGAGGCTTGGAGTCAATTTACTTTTGTGTGTGTGTGTGTGTGTGT
Qy	251	ThrIleGlyPheGlyAspTyPheAlaGlyGly---SerAspIleGluTyPheLeuAspPhe 269
Db	826	ACGGTGGCTTTTGTGATTTTGTGGCAGGGGAAACGCTGGCATCAATTTATCGGAGTGG 885
Qy	270	TyrLysProValValTrpPheTrpIleLeuValGlyLeuAlaTyPheAlaAlaValLeu 289
Db	886	TATAAGCCCTTAGT
Qy	290	SerMetIleGlyAspTrpLeuArgValIleSerLysLysThrLysGluValGlyGlu 309
Db	946	AGTATGATCGGAGATTGGCTACGGGTCTCTCCAAAAAGACAAAGAGAGGTGGGTGAA 1005

Qy	310	PheArgAlaHisAlaAlaGluTrpThrAlaAsnValThrAlaGluPheLysGluThrArg 329
Db	1006	ATCAAGCCCATCGCGCAGAGTGAAGCAATGTACGGTGTAGTTCGGGAGACACGG 1065
Qy	330	ArgArgLeuSerValGluIleTyPheLysPheGlnArgAlaThrSerVal----- 346
Db	1066	CGAAGGCTCAGCGTGGAGATCCACGATAGCTGCAGCGGGCGGCCACCATCGCAGCATG 1125
Qy	347	---LysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365
Db	1126	GAGCGCGCGCGCTGGCGCTGGACACGCGGCCACTCTACTGGACATGTGTCTCCCGCAG 1185
Qy	366	MetArgThr 368
Db	1186	AAGCGCTCT 1194

RESULT 7

US-09-852-386-34

Sequence 34, Application US/09852386

Publication No. US20030064433A1

GENERAL INFORMATION:

APPLICANT: Robert, Steven L.

APPLICANT: Benjamin, Christopher

APPLICANT: Karnovsky, Alla M.

APPLICANT: Ruble, Cara L.

APPLICANT: Ruble, Cara L.

ION CHANNELS

FILE REFERENCE: 00133 US1

CURRENT APPLICATION NUMBER: US/09/852,386

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 60/203,305

PRIOR FILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: 60/207,092

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/206,526

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,033

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/207,093

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/216,893

PRIOR FILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 60/237,873

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: 60/223,245

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 88

SOFTWARE: Patent in version 3.0

SEQ ID NO 34

LENGTH: 1632

TYPE: DNA

ORGANISM: Homo sapiens

US-09-852-386-34

Alignment Scores:	3.42e-125	Length:	1632
Pred. No.:	1247.50	Matches:	247
Score:	78.07%	Conservative:	52
Percent Similarity:	78.07%	Mismatches:	67
Best Local Similarity:	64.49%	Indels:	17
Query Match:	66.25%	Gaps:	5
DB:	10		

US-09-655-272-4 (1-370) x US-09-852-386-34 (1-1632)

Qy	2	AlaAlaProAspLeuLeuAspProLysSerAla-----Ala 13
Db	64	GCAGCAGCACCCTCCCAAGGGGCTTGCAGACCGTCATGAAGTGAAGACGGTGTTCCTCC
Qy	14	GlnAsnSerLysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33
Db	124	CCGACTCCAACTCGGCGCTTGCTTCCTCCGAGCCACAGTGTAGCC---AGGATG 180
Qy	34	GlusSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrile 50





Thu Feb 3 07:31:03 2005

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QY 211 ThrilePheIleLeuPheGlyCysValLeuPheValAlaLeuProAlaValIlePhe 230
Db 733 ACCATCTGTTCATCTGTCGGCGCTGCATTGTTGTGAGCATCCCTGCTCATCTTT 792
QY 231 LysHileIleGluGlyTrpSerAlaLeuAspAlaIleTyPheValValIleThrIleThr 250
Db 793 AAGTACATCGAGGCTTGGAGCGCTTGGAGTCCATTACTTTGTGTGTCTACTCTGACC 852
QY 251 ThrileGlyPheGlyAspTyPheValAlaGlyGly---SerAspIleGluTyPheLeuAspPhe 269
Db 853 ACGGTGGCGCTTGTGATTTGTGGAGCGGGGAAACGCTGGCATCAATATCGGAGTGG 912
QY 270 TyPheProValValTrpPheTrpIleLeuValGlyLeuAlaTyPheAlaValIle 289
Db 913 TATAGCCCTAGTGTGTGTTTGGATCTTGTGGCTTGCCTACTTTGCAGCTGTCTTC 972
QY 290 SerMetIleGlyAspTrpLeuArgValIleSerIleValIleThrIleGluValGlyGlu 309
Db 973 AGTATGATCGAGATTCGCTACCGGTTCTGTCCAAAAGACAAAGAGAGTGGGTGAA 1032
QY 310 PheArgAlaHisAlaAlaGluTrpThrAlaAsnValThrAlaGluPheIleThrArg 329
Db 1033 ATCAAGGCCCATCGGAGAGTGGAGGCCAATGTCAAGGCTGAGTTCGGGGAGACACGG 1092
QY 330 ArgArgLeuSerValGluIleTyPheAspIlePheGlnArgAlaThrSerVal----- 346
Db 1093 CGAAGGCTCAGCTGGAGATCCACGATAAGTCAGCGGGGAGCCACCATCCGACATG 1152
QY 347 ---LysArgIleLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365
Db 1153 GAGCGCGCGCGTGGCGCTGGACGAGCGGCCCACTCACTGGACATGCTGTCCCCCGAG 1212
QY 366 MetArgThr 368
Db 1213 AAGCGCTCT 1221
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RESULT 9  
US-10-262-511-105

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Sequence 105, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Willet, Isabelle
APPLICANT: Feyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Wei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
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CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Curasequid version 0.1
SEQ ID NO 105
LENGTH: 2028
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(1689)
US-10-262-511-105

Alignment Scores:
Pred. No.: 4,68e-125 Length: 2028
Score: 1247.50 Matches: 247
Percent Similarity: 78.07% Conservative: 52
Best Local Similarity: 64.49% Mismatches: 67
Query Match: 66.25% Indels: 17
DB: 16 Gaps: 5

US-09-655-272-4 (1-370) x US-10-262-511-105 (1-2028)
QY 2 AlaAlaProAspLeuLeuAspProLysSerAla-----Ala 13
Db 124 GCAGCAGACCCCGTGTGCCAGCCCAAGAGCGCCACTAACGGGCAACCCCGCGCTCCGCGT 183
QY 14 GlnAsnSerLysProArgLeuSerPheSerLysProThrValLeuAlaSerArgVal 33
Db 184 CCGACTCCAACTCCGCGCTGTCCATTTCTCCGAGCCACAGTGGTAGCC---AGGATG 240
QY 34 GluSerAspSer-----AlaIleAsnValMetLysTrpLysThrValSerThrIle 50
Db 241 GAAGGCACCTCCCAAGGGGGCTTGCAGCCGTCATGAGTGGAGACGGTGGTGGCCATC 300
QY 51 PheLeuValValValLeuTyPheIleLeuGlyAlaAlaValPheIleAlaLeuGluGln 70
Db 301 TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 71 ProGlnGluLeuSerGlnArgThrThrIleValIleGlnLysGlnThrPheIleAlaGln 90
Db 361 CCCTTTGAGAGACGAGCAGAGAAATACATCGCCCTGGAGAGCGGGAATCTCGCGGGAT 420
QY 91 HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnGlnIleValAlaIle 110
Db 421 CATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 111 AsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130
Db 481 AATCGCGGAGTCACTCAATAGGAAACTCTTCCAAACACAGCAGCCACTTGGGACCTCGGC 540
QY 131 SerSerPhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSerPro 150
Db 131 SerSerPhePheAlaGlyThrValIleThrThrIleGlyPheGlyAsnIleSerPro 150
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Qy 270 TyLysProValValTrpPheTrpIleLeuValGlyLeuAlaTyRpheAlaValLeu 289
Db 1358 TATAAGCCCTAGTGTGGTTTGGATCCCTTGTGTGGCCCTGCCTACTTGCAGCTGTCTC 1417
Qy 290 SerMetIleGlyAspTrpLeuArgValIleSerIysIysThrIysGluValGlyGlu 309
Db 1418 AGTATGATCGGAGATTGGCTACCGGGTTCTGTCAAAAAGACAAAGAAGAGGTGGGTGAA 1477
Qy 310 PheArgAlaHisAlaAlaGluTTrpThrAlaAsnValThrAlaGluPheLysGluThrArg 329
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Db 1538 CGAAGGCTCAGCGTGGAGATCCAGATAAGCTGCAGCGGGCGGCCACCATCCGCGCATG 1597
Qy 347 ---LysArgLysLysSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCys 365
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Qy 366 MetArgThr 368
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RESULT 13
US-10-332-447-42
; Sequence 42, Application US/10332447
; Publication No. US20040053258A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
; APPLICANT: TANG, Y.Tom; HARLAND, Lee; BURFORD, Neil;
; APPLICANT: GREENE, Bartie D.; SANJANWALA, Madhu S.;
; APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
; APPLICANT: ARVIZU, Chandra S.; GANDHI, Ameet R.;
; APPLICANT: HAPALIA, April J.A.; TRIBOULEY, Catherine M.;
; APPLICANT: WALIA, Narinder K.; AU-YOUNG, Janice;
; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi;
; APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
; APPLICANT: XU, Yuming; SEILHNER, Jeffrey J.; NGUYEN, Danniell B.;
; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELOU, Kavitha;
; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0149 USN
; CURRENT APPLICATION NUMBER: US/10/332,447
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/216,547
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,232
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,112
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,839
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CB1
US-10-332-447-42

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DB	775	TTTGTGGTGTGGTGTCTACCTTGTCTACCTGGCGGTCTGTCTTCGGGCATTTGGAGCAG 834	
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QY	91	HisAlaCysValAsnSerThrGluLeuAspGluLeuIleGlnIleValAlaIle 110	
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QY	111	AsnAlaGlyIleIleProLeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGly 130	
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QY	131	SerSerPhePheAlaGlyThrValIleThrIleGlyPheGlyAsnIleSerPro 150	
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QY	151	ArgThrGluGlyGlyIlePheCysIleIleIleValAlaLeuLeuGlyIleProLeuPhe 170	
DB	1072	AGCACTGAAGAGGGAATCTTTTGTATTTATATGCACTTTTGGAAATTCACCTCTTT 1131	
QY	171	GlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheGlyLysGlyIleAla 190	
DB	1132	GCTTTCTATTGCTGGAATTTGGAGACCACTTGGAACTCTTGTGGAAAGCAATGCA 1191	
QY	191	LysValGluAspThrPheIleIysTrpAsnValSerGlnThrLysIleArgIleIleSer 210	
DB	1192	AGAGTGGGAAGGTCTTTTCGAAAAAGCAAGTGAAGTCAACAGATCCGGTCACTCA 1251	
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QY	231	LysHisIleGluGlyTrpSerAlaLeuAspAlaIleIlePheValValIleThrLeuThr 250	
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QY	251	ThrIleGlyPheGlyAspThrValAla-----GlyCysSerAspIleGlu 265	
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QY	286	AlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSerLysLysThrLysGlu 305	
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DB	1612	CGGGAGACAGCGGAAGGCTCAGCGTGGAGATCCAGATAAGCTCAGCGGCGACCCACC 1671	
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QY	362	LeuThrProCysMetArgThr 368	
DB	1732	CTGTCCCCCGAGAAGCGCTCT 1752	
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Sequence 1, Application US/10243035			
Publication No. US20030049697A1			
GENERAL INFORMATION:			
APPLICANT: LAZDUNSKI, MICHEL			
APPLICANT: LESAGE, FLORIAN			
APPLICANT: MAINGRET, FRANCOIS			
TITLE OF INVENTION: NEW FAMILY OF MECHANOSENSITIVE HUMAN POTASSIUM CHANNELS			
TITLE OF INVENTION: ACTIVATED BY POLYUNSATURATED FATTY ACIDS AND THEIR USE			
FILE REFERENCE: 1317-02			
CURRENT APPLICATION NUMBER: US/10/243,035			
CURRENT FILING DATE: 2002-09-13			
NUMBER OF SEQ ID NOS: 15			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 1			
LENGTH: 1182			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)..(1179)			
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QY	62	AlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIleVal 81	
DB	61	GCCTGTGTTCGGGCGCTTGGAGCAGCCCGCCAGCAGCAGCGCCAGAGGAGCTGGGG 120	
QY	82	IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101	
DB	121	GAGGTCCGAGAGAAGTCTCTGAGGCGCCATCCGTGTGTGAGCGACGAGAGTGGGCTC 180	
QY	102	LeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121	
DB	181	CTCATCAAGAGGTGGCTGATGCCCTGGGAGGGGTGGGAGCCAGAAACCACTCGACC 240	
QY	122	AsnGlnValSerHis-----TrpAspLeuGlySerSerPhePheAlaGlyThrVal 139	
DB	241	AGCAACAGCAGCCACTCAGCTGGGACCTGGGCGGCTCTTTTCTTCAGGAGCATC 300	
QY	140	IleThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCys 159	
DB	301	ATCACCACTACGCTATGGCAATGTGGCCCTCGCGCAGATGCCGGGCGCTCTTCTGC 360	
QY	160	IleIleThrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAsp 179	
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QY 200 AsnValSerGlnThrLysIleArgIleSerThrIlePheIleLeuPheGlyCys 219
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Db 481 CAGTGCACCGGAGCTAGTAAGAGTGTCTGGCGATGTTCTTCTGCTGATCGGCTGC 540
QY 220 ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTyrSerAlaLeu 239
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QY 240 AsnAlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAla 259
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QY 260 GlyGlySerAspIleGluTyrLeuAspPheTyrLysProValValTyrPheTyrIleLeu 279
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QY 280 ValGlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTyrLeuArgValIle 299
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QY 300 SerLysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTyrThrAla 319
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## RESULT 15

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; Sequence 3, Application US/09828035
; Patent No. US20020034781A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 12303, A NOVEL HUMAN TWIK MOLECULE AND USES THEREOF
; FILE REFERENCE: WNI-142
; CURRENT APPLICATION NUMBER: US/09/828,035
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,734
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1257)
US-09-828-035-3
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Score: 797.00 Matches: 145
Percent Similarity: 72.18% Conservative: 60
Best Local Similarity: 51.06% Mismatches: 77
Query Match: 42.33% Indels: 2
DB: 9 Gaps: 1
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QY 122 AsnGlnValSerHis-----TyrAspLeuGlySerSerPhePheAlaGlyThrVal 139
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GenCore version 5.1.6  
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63: /cgn2\_6/ptodata/1/pna/US108B\_COMB.seq:  
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65: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq:  
66: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq:  
67: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq:  
68: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq:  
69: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq:  
70: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq:  
71: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq:  
72: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq:  
73: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq:  
74: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq:  
75: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq:  
76: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq:  
77: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq:  
78: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq:  
79: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq:  
80: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq:  
81: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq:  
82: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq:  
83: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq:  
84: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq:  
85: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq:  
86: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq:  
87: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq:  
88: /cgn2\_6/ptodata/1/pna/US6023A\_COMB.seq:  
89: /cgn2\_6/ptodata/1/pna/US6023B\_COMB.seq:  
90: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq:  
91: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq:  
92: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq:  
93: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq:  
94: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq:  
95: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq:  
96: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq:  
97: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq:  
98: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq:  
99: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq:  
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101: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq:

102: /cgn2\_6/ptodata/1/pna/US6036 COMB.seq.\*  
 103: /cgn2\_6/ptodata/1/pna/US6037 COMB.seq.\*  
 104: /cgn2\_6/ptodata/1/pna/US6038 COMB.seq.\*  
 105: /cgn2\_6/ptodata/1/pna/US6039 COMB.seq.\*  
 106: /cgn2\_6/ptodata/1/pna/US6040 COMB.seq.\*  
 107: /cgn2\_6/ptodata/1/pna/US6041 COMB.seq.\*  
 108: /cgn2\_6/ptodata/1/pna/US6042 COMB.seq.\*  
 109: /cgn2\_6/ptodata/1/pna/US6043 COMB.seq.\*  
 110: /cgn2\_6/ptodata/1/pna/US6044 COMB.seq.\*  
 111: /cgn2\_6/ptodata/1/pna/US6045 COMB.seq.\*  
 112: /cgn2\_6/ptodata/1/pna/US6046 COMB.seq.\*  
 113: /cgn2\_6/ptodata/1/pna/US6047 COMB.seq.\*  
 114: /cgn2\_6/ptodata/1/pna/US6048 COMB.seq.\*  
 115: /cgn2\_6/ptodata/1/pna/US6049 COMB.seq.\*  
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 117: /cgn2\_6/ptodata/1/pna/US6051 COMB.seq.\*  
 118: /cgn2\_6/ptodata/1/pna/US6052 COMB.seq.\*  
 119: /cgn2\_6/ptodata/1/pna/US6053 COMB.seq.\*  
 120: /cgn2\_6/ptodata/1/pna/US6054 COMB.seq.\*  
 121: /cgn2\_6/ptodata/1/pna/US6055 COMB.seq.\*  
 122: /cgn2\_6/ptodata/1/pna/US6056 COMB.seq.\*  
 123: /cgn2\_6/ptodata/1/pna/US6057 COMB.seq.\*  
 124: /cgn2\_6/ptodata/1/pna/US6058 COMB.seq.\*  
 125: /cgn2\_6/ptodata/1/pna/US6059 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1870	99.3	1994	34	US-09-828-746-5
2	1870	99.3	1994	45	Sequence 37, Appl
3	1864	99.0	3580	22	US-10-036-657-37
4	1833	97.3	1236	22	US-09-503-089A-3
5	1833	97.3	1246	34	US-09-503-089A-1
6	1833	97.3	1246	44	US-09-828-746-1
7	1833	97.3	1246	44	US-09-980-350-1
8	1833	97.3	3300	47	US-10-036-657-35
9	1833	97.3	3316	1	PCT-US99-03826-82
10	1829	97.1	3256	48	US-10-170-235-27467
11	1829	97.1	3256	110	US-60-443-566-876
12	1829	97.1	3256	111	US-60-455-444-3496
13	1829	97.1	3256	112	US-60-465-241-3496
14	1827	97.0	2391	2	PCT-US03-01911-9
15	1827	97.0	2391	51	US-10-349-528-9
16	1805	95.9	2130	13	US-08-816-011-46
17	1805	95.9	2130	13	US-08-816-011A-46
18	1805	95.9	2130	13	US-08-816-011C-46
19	1805	95.9	2130	13	US-08-816-011E-46
20	1805	95.9	2130	13	US-08-816-011F-46
21	1805	95.9	2130	13	US-08-816-011G-46
22	1805	95.9	2130	22	US-09-503-849B-46
23	1805	95.9	2130	22	US-09-503-849D-46
24	1801	95.6	2130	22	US-09-503-849B-61
25	1801	95.6	2130	22	US-09-503-849D-61
26	1800	95.6	2130	22	US-09-503-849B-62
27	1800	95.6	2130	22	US-09-503-849D-62
28	1797	95.4	2130	22	US-09-503-849B-64
29	1797	95.4	2130	22	US-09-503-849D-64
30	1796	95.4	2130	22	US-09-503-849B-63
31	1796	95.4	2130	22	US-09-503-849D-63
32	1743.5	92.6	3393	54	US-10-473-305-346
33	1589.5	84.4	2496	61	US-10-760-320A-439
34	1589.5	84.4	2496	61	US-10-760-320A-439
35	1447	76.8	1702	2	PCT-US03-24164-70
36	1365	72.5	2793	47	US-10-144-771-3874
37	1365	72.5	2793	102	US-60-360-207-3874
38	1252.5	66.5	2126	47	US-10-144-771-12647
39	1252.5	66.5	2126	102	US-60-360-207-12647

Sequence 1, Appli  
 Sequence 34, Appl  
 Sequence 34, Appl  
 Sequence 1, Appli  
 Sequence 470, App  
 Sequence 771, App

ALIGNMENTS

RESULT 1  
 US-09-828-746-5  
 ; Sequence 5, Application US/09828746  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Helen Jane Meadows  
 ; APPLICANT: Conrad Gerald Chapman  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP-30031-DI  
 ; CURRENT APPLICATION NUMBER: US/09/828,746  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 09/236,080  
 ; PRIOR FILING DATE: 1999-01-25  
 ; PRIOR APPLICATION NUMBER: EP 98300570.3  
 ; PRIOR FILING DATE: 1998-01-27  
 ; PRIOR APPLICATION NUMBER: UK 9822135.1  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1994  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-828-746-5

Alignment Scores:  
 Pred. No.: 3.1e-197 Length: 1994  
 Score: 1870.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.31% Indels: 0  
 DB: 34 Gaps: 0

US-09-655-272-4 (1-370) x US-09-828-746-5 (1-1994)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 DB 484 AUGCGCGCCCTGACTTGTGGATCCAGTCTGCTCAGACTCCAAACCGAGGCTC 543  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 DB 544 TCATTCTTCAAAACCCACCGTGTGCTTCCCGGGTGGAGAGTACTCGGCCATTAT 603  
 QY 41 ValMetLysTrpLysThrValSerThrLysPheLeuValValLeuTrpLeuLeuLe 60  
 DB 604 GTTATCAAAATGGAAGACAGTCTCCACGATTTTCCTGGTGGTCTCTACCTGATCATC 663  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrThrile 80  
 DB 664 GAGGCCCGCGGTGTTCAGGCATTTGGAGAGCCCTCAGAGATTTCCAGAGGACCACCAIT 723  
 QY 81 ValileGlnLysGlnThrPheLeAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 DB 724 GTGATCCAGAAGCAGACACCTTCATAGCCAGCATGCTGGCTCAACTCCACCGAGCTGGAC 783  
 QY 101 GluLeuLeuGlnGlnLeuValAlaAlaLeuAsnAlaGlyLeuLeuProLeuGlyAsnSer 120  
 DB 784 GAACATCATCAGCAATAGTGGCAGCAATAAAGCAGGAGATTTATCCCTTAGGAACAGC 843  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValile 140  
 DB 844 TCCAAATCAAGTAGTACTGCTGGAGCTCCGAGAGCTCTTTCTTCTTGTGTACTGTATC 903  
 QY 141 ThrThrileGlyPheGlyAsnileSerProArgThrGluGlyLyslePheCysile 160

```
Db 904 ACAACCATGAGTTGGAAACATCTCCCAACGAACTGAAGTGGAAATATTTCTGCATC 963
Qy 161 ILeTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 964 ATCTATGCTTGTGGGAATTCCTCTTTGGCTTCTACTGCTGGGTGGTGATCAG 1023
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 1024 CTAGGAATATATTTGGAAAGAAATTCGCAAGTGGAAACACATTTATTAAGTGAAT 1083
Qy 201 ValSerGlnThrIysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1084 GTTAGTCAGACGAAGATTCGTATCATCTCCACCATCATCTTCATCTGTTGGCTGGTC 1143
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 1144 CTCTTTGTGCTCTCCCTGGCTCATATTCACGACATAGAGGCTGGAGCGCCTGGAC 1203
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 1204 GCTATCTATTTGTGGTTATCACTCTGACGACCATTCGATTTGGAGACTACGTGGCAGGT 1263
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrIysPheTrpValValThrPheTrpIleLeuVal 280
Db 1264 GSATCAGACATTAATATCTGGACTTCTACAAGCCTGTGGTGGTTCTGGATCCTCGTT 1323
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 1324 GGCTGGCTTACTTTGACGCTGTCTGAGCATGATNTGGGACTGGCTACGGGTGATCTCT 1383
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 1384 AAGAAGCAAGGAAGAGGTGGAGAGTTCAGAGCGCATCCGCTGAGTGGACAGCCAAAT 1443
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1444 GTCACGGCCGAGTTCAGGAACAGAGAGCGGCTGAGCGTGGAGATCTACGCAAGATTC 1503
Qy 341 GluArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1504 CAGGTGCCACATCCGTGAAGCGGAGCTCTCCGAGAGCTGGCGGCAACCAACACAG 1563
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1564 GAACTGACTCCGTGTATGAGGACC 1587
```

## RESULT 2

```
US-10-036-657-37
; Sequence 37, Application US/10036657
; GENERAL INFORMATION:
; APPLICANT: Earl Francis Albone, et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: GP-70778B-CI
; CURRENT APPLICATION NUMBER: US/10/036,657
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-036-657-37
```

```
Alignment Scores:
Pred. No.: 3,1e-197 Length: 1994
Score: 1870.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.31% Indels: 0
DB: 45 Gaps: 0
```

US-09-655-272-4 (1-370) x US-10-036-657-37 (1-1994)

```
Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu 20
Db 484 ATGGCGGCCCTGACTGCTGGATCCAGTCTGCTCAGAACTCCAAACCGAGGCTC 543
Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 544 TCATTTCTTTCAAAACCCACCGCTGCTTCCCGGTGGAGAGTGACTCGGCATTAAT 603
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuTyrLeuIleIle 60
Db 604 GTTATGAATGGAAGACAGCTCTCCAGATTTTCTGGTGGCTGCTCTTACCTGATCATC 663
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLysSerGlnArgThrThrIle 80
Db 664 GGAGCGCGCTGTTCAGGCAATTTGGAGCAGCTTCAGAGATTTCCAGAGAGCACCATTT 723
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp 100
Db 724 GTGATCCAGAAAGCAGACCTTCATAGCCCGCAGCATGCTGCGTCAACTCCACGAGCTGGAC 783
Qy 101 GluLeuIleGlnLysIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 784 GAACTCATCCAGCAATATAGTGGCAGCAATAAAGCGAGGATTAATCCCTTAGGAAACAGC 843
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 844 TCCAAATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTTCTTCTGCTGCTGTTATC 903
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
Db 904 ACAACATATAGGATTTGGAAACATCTCCCAACGAACTGAAGGTGGAAATATTTCTGCATC 963
Qy 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 964 ATCTATGCTTGTGGGAATTCCTCTTTGGCTTCTACTGCTGGGTGGTGATCAG 1023
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 1024 CTAGGAATATATTTGGAAAGAAATTCGCAAGTGGAAACACATTTATTAAGTGAAT 1083
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1084 GTTAGTCAGACGAAGATTCGTATCATCTCCACCATCATCTTCATCTGTTGGCTGGTC 1143
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 1144 CTCTTTGTGCTCTCCCTGGCTCATATTCAGCAATAGAGGCTGGAGCGCCTGGAC 1203
Qy 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 1204 GCTATCTATTTGTGGTTATCACTCTGACGACCATTTGGATTTGGAGACTACGTGGCAGGT 1263
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValThrPheTrpIleLeuVal 280
Db 1264 GGATCAGACATTAATATCTGGACTTCTACAAGCCTGTGGTGGTTCGTGATCCTCGTT 1323
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 1324 GGGCTGGCTTACTTTGACGCTGTTCTGAGCATGATNTGGGACTGGCTACGGGTGATCTCT 1383
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 1384 AAGAAGCAAGGAAGAGGTGGAGAGTTCAGAGCGCATCCGCTGAGTGGACAGCCAAAT 1443
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1444 GTCACGGCCGAGTTCAGGAACAGAGAGCGGCTGAGCGTGGAGATCTACGCAAGATTC 1503
Qy 341 GluArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1504 CAGGTGCCACATCCGTGAAGCGGAGCTCTCCGAGAGCTGGCGGCAACCAACACAG 1563
```



US-09-655-272-4 (1-370) x US-09-503-089A-1 (1-1236)

```
QY 1 MetAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 1 ATGGCGGCCCTGACTGCTGGATCCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 60
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 61 TCGTTTTCCAGAAACCCAGAGCTGCTTCCCGGGTGAGAGTGACACGACCATTAAT 120
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIleIle 60
Db 121 GTTATGAAATGGAAGACGGTCTCAGATATTCCTGGTGTGCTCTATCTGATCATC 180
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
Db 181 GGAGCCACCGTGTTCAGAACATTTGGAGCAGCCTCATGAGATTTTCACAGAGCACCAT 240
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 241 GTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 300
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 301 GAACATTCATCAGCAATATGCGGACGACATTAATGACGGATTAATCCGTTAGGAACACC 360
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 361 TCCAATCAATCAGTCAGTGGATTTGGGAAGTTCTCTTCTTCTGCTGGCACTGTTATT 420
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
Db 421 ACAACCATAGGATTTGGAAACATCTCACCAACGACAGAGCGGCAAAATATTTCTGTATC 480
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
Db 481 ATCTATGCTTACTGGAAATCCCTCTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 540
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 541 CTAGGCACCATATTTGGAAAGGAATGCCAAGTGGAGATACGTTTATTAAGTGGAAAT 600
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 601 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATCTATTTGGCTGTGTA 660
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 661 CTCTTTGTGGCTCTGCTGGATCATATTCAAACACATAGAGGCTGGAGTGCCTGGAC 720
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 721 GCCATTTATTTTGGTTATCACTCTAACAACTATTGGATTGGTACGTTGACGTTGAGGT 780
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 781 GGATCCGATATCAATATCTGGACTTCTATAAGCCTGCTGTGTGGTTCTGGATCCTTGTA 840
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 841 GGGCTTGTCTTACTTGTCTGCTGCTGAGATGATTTGGAGATTTGGCTCCGAGTGATATCT 900
QY 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 901 AAAAGACAAAAGAGGTTGGAGAGTTTCAGAGCACACGCTCTGAGTGGACAGCCAC 960
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 961 GTCACAGCCGAATTCAAAGAAACAGGAGCGAGTGTGAGATTTATGACAAAGTTC 1020
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1021 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGCAGAACTGGCTGGAAACCAATACAG 1080
```

```
QY 361 GluLeuThrProCysMetArgThr 368
Db 1081 GAGTCGACTCCTTGTAGGAGGACC 1104
```

## RESULT 5

```
US-09-828-746-1
; Sequence 1, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-828-746-1
```

## Alignment Scores:

```
Pred. No.: 2,216-193 Length: 1246
Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservative: 8
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 34 Gaps: 0
```

US-09-655-272-4 (1-370) x US-09-828-746-1 (1-1246)

```
QY 1 MetAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 9 ATGGCGGCCCTGACTGCTGGATCCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 68
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 69 TCGTTTTCCAGAAACCCAGAGCTGCTTCCCGGGTGAGAGTGACACGACCATTAAT 128
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIleIle 60
Db 129 GTTATGAAATGGAAGACGGTCTCAGATATTCCTGGTGTGCTCTATCTGATCATC 188
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
Db 189 GGAGCCACCGTGTTCAGAACATTTGGAGCAGCCTCATGAGATTTTCACAGAGCACCAT 248
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 249 GTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 308
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 309 GAACATTCATCAGCAATATGCGGACGACATTAATGACGGATTAATCCGTTAGGAACACC 368
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 369 TCCAATCAATCAGTCAGTGGATTTGGAGAGTTCTCTTCTTCTGCTGGCACTGTTATT 428
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIle 160
Db 429 ACAACCATAGGATTTGGAAACATCTCACCAACGACAGAGGCGGCAAAATATTTCTGTATC 488
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuAlaGlyValGlyAspGln 180
```

```
Db 489 ATCTATGCTTACTTGGGAATCCCTCTTTGGTTTCTTTGGCTGGAGTTGGAGATCAG 548
Qy 181 LeuGlyThrIlePheGlyValAlaGlyValGluAspThrPheIleLeuVal 200
Db 549 CTAGGCACCAATTTGGAAAGGAATTCGAAGTGGAGATACGTTTATTAAAGTGAAT 608
Qy 201 ValSerGlnThrIlePheGlyValAlaGlyValGluAspThrPheIleLeuVal 220
Db 609 GTTAGTCAGACCAAGATTCGATCATCTCAACAATCATATTTATATCTTTGGCTGTGTA 668
Qy 221 LeuPheValAlaLeuProAlaValIlePheLeuHisIleGluGlyTrpSerAlaLeuAsp 240
Db 669 CTCCTTTGGCTCTGGCTGGATCATATTCAAACATAGAGGCTGGAGTCCCTGGAC 728
Qy 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260
Db 729 GCCATTTATTTTGGTTATCACTCTCAACAATATTGGATTTGGTGACCTACGTTGCAGGT 788
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 789 GGATCCGATATTGAATATCTGGACTTCTATTAAGCCTGTCTGGTGTCTGGATCTCTGTA 848
Qy 281 GlyLeuAlaTyrPheAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 849 GGGCTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
Qy 301 LysLysThrLysGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 909 AAAAAGACAAAGAGAGTGGAGAGTTCCAGAGCACACCTCTGAGTGGACAGCAAC 968
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 969 GTACAGCCGAATTCNAAGAAACAGAGGCGAGTGGATGGCTCCGAGTGATATCT 1028
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1029 CAGGGGCGCACTCCATCAGCGAGCTCTGGCAGAACTGGCTGGAACCAACATCAG 1088
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1089 GAGCTGACTCTCTAGGAGGACC 1112
```

```
RESULT 6
US-09-980-350-1
; Sequence 1, Application US/09980350
; GENERAL INFORMATION:
; APPLICANT: HERVIEU, GUILLAUME JEAN
; APPLICANT: MEADOWS, HELEN JANE
; APPLICANT: RANDALL, ANDREW DAVID
; TITLE OF INVENTION: USES OF H-TREK-1 POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: P32320
; CURRENT APPLICATION NUMBER: US/09/980,350
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/GB00/02107
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: GB 9912733.4
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-980-350-1

Alignment Scores:
Pred. No.: 2,21e-193 Length: 1246
Score: 1633.00 Matches: 356
Percent Similarity: 98.91% Conservative: 8
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 44 Gaps: 0
```

```
US-09-655-272-4 (1-370) x US-09-980-350-1 (1-1246)
Qy 1 MetAlaIaIaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 9 ATGCGCGACCTGACTTGGTGGATCTTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC 68
Qy 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 69 TCGTTTTCCAGAAACCCACAGTGTCTTCCGGGTGGAGAGTGACACGCAATTAAT 128
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIle 60
Db 129 GTTATGAAATGGAAGACGGTCTCCACGATATTCCTGGTGGTGTCTCTATCTGATCATC 188
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80
Db 189 GGAGCCACCGGTGTTCAAGCATTTGGAGCGCTCATGAGATTTTCACAGAGGACCACTT 248
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 249 GTGATCCAGAGCAACATTCATATCCCAATTCCTGTGTCTCAATTCGAGCGAGCTGGAT 308
Qy 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 309 GAACCTCATTCAGCAAAATAGTGGCAGCAATAAATGAGGAGATTATACCGTTAGGAAACAC 368
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 369 TCCATCAANTCAGTCACTGGGATTTGGGAATTCCTTCTTCTTCTGGCAGCTGTATT 428
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysVal 160
Db 429 ACAACCATAGGATTTGGAAACATCTCACACGACAGAAAGCGGCAAAATATCTGTATC 488
Qy 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 489 ATCTATGCTTACTTGGGAATTCCTCTTGGTTCTTCTTGGCTGGAGTTGGAGATCAG 548
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 549 CTAGGCACCAATTTTGGAAAGGAATTCGAAGTGGAGATACGTTTATTAAAGTGAAT 608
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 609 GTTAGTCAGACCAAGATTTGGCATCATCTCAACAATCATATTTATATCTTTGGCTGTGTA 668
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 669 CTCCTTTGGCTCTGGCTGGATCATATTCAAACACATAGAGGCTGGAGTCCCTGGAC 728
Qy 241 AlaIleTyrPheValValIleThrLeuThrIleGlyPheGlyAspTyrValAlaGly 260
Db 729 GCCATTTATTTTGGTGTATCATCTCAACAATATTGGATTTGGTGACTACCTGTCAGGT 788
Qy 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 789 GGATCCGATATTGAATATCTGGACTCTATAGCCTGCTGCTGGTCTGGATCTCTGTA 848
Qy 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 849 GGGCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 909 AAAAAGACAAAGAGAGTGGAGAGTTCCAGAGCACACGCTGCTGAGTGGAGCAAC 968
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 969 GTACAGCCGAATTCNAAGAAACAGAGGCGAGTGGATGGCTCCGAGTGATATCT 1028
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1029 CAGGGGCGCACTCCATCAGCGAGCTCTGGCAGAACTGGCTGGAACCAACATCAG 1088
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Db 1029 CAGCGGGCCACCTCCATCAGCGGAAGCTCTCGCAGAACTGCTGGAAACCAATCAG 1088
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1089 GAGCTGACTCTTGTAGGAGACC 1112
RESULT 7
US-10-036-657-35
; Sequence 35, Application US/10036657
; GENERAL INFORMATION:
; APPLICANT: Earl Francis Albone, et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: GP-707788-CL
; CURRENT APPLICATION NUMBER: US/10/036,657
; PRIORITY FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-036-657-35
Alignment Scores:
Pred. No.: 2,21e-193 Length: 1246
Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservative: 4
Best Local Similarity: 96.74% Mismatches: 4
Query Match: 97.34% Indels: 0
DB: 45 Gaps: 0
US-09-655-272-4 (1-370) x US-10-036-657-35 (1-1246)
Qy 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 9 ATGGCGGACCTGACTTGTGGATCTCTAAATCTCGCGCTCAGAACTCCAAACCGAGGCTC 68
Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 69 TCGTTTCCAGAAACCCACAGTGTCTTCCCGGGTGGAGAGTGACACGACCAATTAAT 128
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuThrIleIle 60
Db 129 GTTATGAATGGAAGACGGTCTCCAGATATTCCTGGTGGTCTCTCTATCTGATCATC 188
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80
Db 189 GGAGCCACCGTGTTCAGAGCTTGGAGCAGCTCATGAGATTTTCAGAGGACCACTT 248
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 249 GTGATCCAGAAGCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 308
Qy 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 309 GAATCATTCAGCAATATAGTGGCAGCAATAAATAGCAGGATTTATACCGTTAGGAACACC 368
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 369 TCCAAATCAATCAGTCACTGGGATTTGGAGAGTCTCTCTTCTGCTGGCACTGTATT 428
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
Db 429 ACAACCATAGGATTTGAAACATCTCCACAGCAGACAGAGCGGCAAAATATTCGTATC 488
Qy 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 489 ATCTATGCTCTTACTGGGAATTCCTCTTTGGTTTCTCTTGGCTGGAGTTGGAGATCAG 548
Qy 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 549 CTAGGCGCACCATATTTGGAAAGGAATTCGCCAAAGTGGAGATACGTTTATTAAAGTGAAT 608
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Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 609 GTTAGTCAGCAAGATTCGCATCATCTCAACAATCATATTTATATCTATTTGGCTGTGTA 668
Qy 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 669 CTCCTTGTGGCTCTGCTGCGATCATATTCAACACATAGAGGCTGGAGTGGCCTGGAC 728
Qy 241 AlaIleTyPheValValIleThrLeuThrIleGlyPheGlyAspTyTrpValAlaGly 260
Db 729 GCCATTTATTTTGGTGTATCATCTCAACAATCTATTTGGATTTGGTACTACGTTGCAGGT 788
Qy 261 GlySerAspIleGluTyLysAspPheTyLysProValValTrpPheTrpIleLeuVal 280
Db 789 GGATCCGATATTGAATATCTGACCTCTATAAGCCCTGTCTGTGGTCTCGGATCCTTGTGA 848
Qy 281 GlyLeuAlaTyPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 849 GGGCTTGTCTTACTTTGCTGCTCTGACGATGATTTGGAGATTTGGCTCGAGTGATATCT 908
Qy 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 909 AAAAAGACAAAGAGAGGCTGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCAAC 968
Qy 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyTrpAspLysPhe 340
Db 969 GTACAGCGCGAATTCAAAGAAACCCAGAGGCGCAGTGTGAGATTTATGCAAGTTTC 1028
Qy 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1029 CAGCGGCGCACCTCCATCAAGCGGAAGCTCTCGCAGAACTGCTGGAAACCAATCAG 1088
Qy 361 GluLeuThrProCysMetArgThr 368
Db 1089 GAGCTGACTCTTGTAGGAGGACC 1112
RESULT 8
US-10-121-746-82
; Sequence 82, Application US/10121746
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-07
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50) ... (1285)
US-10-121-746-82
Alignment Scores:
Pred. No.: 8,31e-193 Length: 3300
Score: 1833.00 Matches: 356
Percent Similarity: 98.91% Conservative: 8
Best Local Similarity: 96.74% Mismatches: 4
```

Query Match: 97.34% Indels: 0  
DB: 47 Gaps: 0

US-09-655-272-4 (1-370) x US-10-121-746-82 (1-3300)

QY 1 MetAlaAlaProAspLeuLeuValSerProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 50 ATGGGGACCTGACCTGCTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 109

QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 110 TCGTTTCCAGAAACCCAGAGCTGCTTCCCGGTGGAGAGTGCACAGCCATTAAT 169

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIle 60  
DB 170 GTTATGAATGGAGAGCGTCTCAGATATCTGCTGGTGTCTCTCTATCTGATCATC 229

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
DB 230 GGAGCCACCGTGTCAAAGCATTGGAGCAGCTCATGAGATTTTCAGAGGACCCATT 289

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 290 GTGATCCAGAAACCAATCATATCCCAATTCCTGTGTCAATTCGAGCGAGCTGGAT 349

QY 101 GluLeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 350 GAATCATTCAGCAATAGTGGAGCAATTAATAGCAGGATTAATCCGTTAGGAACACC 409

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 410 TCCAATCAATCAGTCACTGGGATTTGGGAAGTTCCTTCTTCTTCTGCTGCTGCTTATT 469

1010 GTACAGCCGAATTCAGAAACCAAGGAGGAGCTGAGTGTGGAGATTTATGACAGTTC 1069

QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
DB 1070 CAGCGGCGACCTCCATCAGCGGAAGCTCTCGGAGAACTGGCTGGAAACCAATCAG 1129

QY 361 GluLeuThrProCysMetArgThr 368  
DB 1130 GAGCTGACTCTCTTGTAGGAGGCC 1153

RESULT 9

PCT-US99-03826-82

Sequence 82, Application PC/TUS9903826A

GENERAL INFORMATION:

APPLICANT: Miller, Andrew

APPLICANT: Curran, Mark

TITLE OF INVENTION: Novel Human Potassium Channels

FILE REFERENCE: SEQ-15PCT

CURRENT APPLICATION NUMBER: PCT/US99/03826A

CURRENT FILING DATE: 1999-02-22

EARLIER APPLICATION NUMBER: 60/076,687

EARLIER FILING DATE: 1998-02-25

EARLIER APPLICATION NUMBER: 60/095,836

EARLIER FILING DATE: 1998-08-07

EARLIER APPLICATION NUMBER: 60/116,448

EARLIER FILING DATE: 1999-01-19

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 82

LENGTH: 3300

TYPE: DNA

ORGANISM: H. sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (50)...(1285)

PCT-US99-03826-82

Alignment Scores:

Pred. No.: 8,36e-193 Length: 3316

Score: 1833.00 Matches: 356

Percent Similarity: 98.91% Conservative: 8

Best Local Similarity: 96.74% Mismatches: 4

Query Match: 97.34% Indels: 0

DB: 1 Gaps: 0

US-09-655-272-4 (1-370) x PCT-US99-03826-82 (1-3316)

QY 1 MetAlaAlaProAspLeuLeuValSerProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
DB 50 ATGGGGACCTGACCTGCTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 109

QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
DB 110 TCGTTTCCAGAAACCCAGAGCTGCTTCCCGGTGGAGAGTGCACAGCCATTAAT 169

QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuValLeuIle 60  
DB 170 GTTATGAATGGAGAGCGTCTCCAGATATTCCTGGTGTGCTCTCTATCTGATCATC 229

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80  
DB 230 GGAGCCACCGTGTCAAAGCATTGGAGCAGCTCATGAGATTTTCAGAGGACCCATT 289

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
DB 290 GTGATCCAGAAACCAATCATATCCCAATTCCTGTGTCAATTCGAGCGAGCTGGAT 349

QY 101 GluLeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
DB 350 GAATCATTCAGCAATAGTGGAGCAATTAATAGCAGGATTAATCCGTTAGGAACACC 409

QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
DB 410 TCCAATCAATCAGTCACTGGGATTTGGGAAGTTCCTTCTTCTTCTGCTGCTGCTTATT 469



QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyIlePheCysIle 160  
Db 470 ACAACCATAGGATTTGGAAACATCTCACACGACAGCGCGCAAAATATTCTGTATC 529  
QY 161 IleTyAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
Db 530 ATCTATGCCCTTACTGGGAATCCCTCTTTGGTTTTCTTTGGCTGGAGTTGGAGATCAG 589  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
Db 590 CTAGGCACCATATTGGAAAGGAATTTGCCAAAGTGGAGATACGTTTATTAAAGTGGAAAT 649  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
Db 650 GTTAGTCAGACCAAGATTCGATCATCTCAACATCATATTTATATCTATTGGCTGTGTA 709  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
Db 710 CTCTTTGTGGCTCTGCTCGATCATATTTCAACACATAGAGGCTGGAGTGCCTGGAC 769  
QY 241 AlaIleTyRPhValValIleThrLeuThrThrIleGlyPheGlyAspTyRValAlaGly 260  
Db 770 GCCATTTATTTGTGGTTATCACTCTAAACAACTATTGGATTGGTGACTACGTTGCAGGT 829  
QY 261 GlySerAspIleGluTyRLeuAspPheTyRLeuProValValTrpPheTrpIleLeuVal 280  
Db 830 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGGTTCTGGATCCTTGTGA 889  
QY 281 GlyLeuAlaTyRPhAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 890 GGGCTTGTCTTACTTGTCTGCTCGATCATATTGGAGATTGGCTCCGAGTGATATCT 949  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
Db 950 AAAAGACAAAGAGAGGTGGAGAGTTCCAGAGCACACCTCTGCTGAGTGGACAGCCAAAC 1009  
QY 321 ValThAlaGluPheLysGluThrArgArgLeuSerValGluIleTyRAspLysPhe 340  
Db 1010 GTCACAGCCCAATTCAAAGAAACAGAGGCGACTGAGTGTGGAGATTTATGCAAGTTTC 1069  
QY 341 GluArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1070 CAGCGGCCACCTCCATCAGCGGAGCTCTCGCAGAACTGGCTGGAAACCAATATCAG 1129  
QY 361 GluLeuThrProCysMetArgThr 368  
Db 1130 GAGCTGACTCTTGTAGGAGGACC 1153

## RESULT 10

US-10-170-235-27467  
; Sequence 27467, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; FILE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
; FILE REFERENCE: CL001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 27467  
; LENGTH: 3256  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-27467

## Alignment Scores:

Pred. No.:	2,28e-192	Length:	3256
Score:	1829.00	Matches:	355
Percent Similarity:	98.91%	Conservative:	9
Best Local Similarity:	96.47%	Mismatches:	4
Query Match:	97.13%	Indels:	0
DB:	48	Gaps:	0

US-09-655-272-4 (1-370) x US-10-170-235-27467 (1-3256)  
QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
Db 64 GTGGCGGACCTGACTTGTGGATCTCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 123  
QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
Db 124 TCGTTTTCACGAAACCCACAGTGTCTCCCGGTGGAGAGTGCACACGACCAATTAAT 183  
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIleIle 60  
Db 184 GTTATGAAATGGAGACGCTCTCCACATATCTCTGGTGTGTCTCTATCTGATCATC 243  
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
Db 244 GGAGCCACCGTGTTCAAAGCATTTGGAGACGCTCATGAGATTTTCACAGAGGACCACT 303  
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
Db 304 GTGATCCAGAAACCAACATTCATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGAT 363  
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
Db 364 GAACTCATTCGCAAAATAGTGGAGCAATTAATGCGAGGATTAATCCGTTAGGAAACACC 423  
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
Db 424 TCCAATCAAAATCAGTCACCTGGGATTTGGGAAGTTCCTCTCTCTTCTGGCACTGTATT 483  
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
Db 484 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGCGCGCAAAATATTCTGTATC 543  
QY 161 IleTyRAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
Db 544 ATCTATGCTTACTGGGAATTCCTCTCTTGGTTTTCTCTGGCTGGAGTTGGAGATCAG 603  
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
Db 604 CTAGGCACCATATTGGAAAGGAATTCGCAAGTGGAAAGATACGTTTATTAAAGTGGAAAT 663  
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
Db 664 GTTAGTCAGACCAAGATTCGATCATCTCAACAAATCATATTTATATCTATTGGCTGTGTA 723  
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240  
Db 724 CTCTTTGTGGCTCTGCTCGATCATATTCAAAACATAGAGGCTGGAGTGCCTGGAC 783  
QY 241 AlaIleTyRPhValValIleThrLeuThrThrIleGlyPheGlyAspTyRValAlaGly 260  
Db 784 GCCATTTATTTGTGGTTATCACTCTAAACATATTGGATTTGGTGCATACGTTGCAGGT 843  
QY 261 GlySerAspIleGluTyRLeuAspPheTyRLeuProValValTrpPheTrpIleLeuVal 280  
Db 844 GGATCCGATATTGAATATCTGGACTTCTATAAGCCTGTCTGTGGTTCTGGATCCTTGTGA 903  
QY 281 GlyLeuAlaTyRPhAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300  
Db 904 GGGCTTGTCTTACTTGTCTGTCTGCTGATGATTTGGAGATTGGCTCCGAGTGATATCT 963  
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
Db 964 AAAAGACAAAGAGAGGTGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCCAAAC 1023  
QY 321 ValThAlaGluPheLysGluThrArgArgLeuSerValGluIleTyRAspLysPhe 340  
Db 1024 GTCACAGCGCAATTCAAAGAAACAGAGGCGCACTGAGTGTGGAGATTTATGCAAGTTTC 1083  
QY 341 GluArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360  
Db 1084 CAGCGGCCACCTCCATCAGCGGAGGAGCTCTCGCAGAACTGGCTGGAAACCAATATCAG 1143

QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1144 GAGCTGACTCTTGTAGGAGGACC 1167

RESULT 11

US-60-443-566-876  
 ; Sequence 876, Application US/60443566  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: BEGOVICH, Ann  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001447  
 ; CURRENT APPLICATION NUMBER: US/60/443,566  
 ; CURRENT FILING DATE: 2003-01-30  
 ; NUMBER OF SEQ ID NOS: 25102  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 876  
 ; LENGTH: 3256  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-60-443-566-876

Alignment Scores:  
 Pred. No.: 2,286-192 Length: 3256  
 Score: 1829.00 Matches: 355  
 Percent Similarity: 98.91% Conservative: 9  
 Best Local Similarity: 96.47% Mismatches: 4  
 Query Match: 97.13% Indels: 0  
 Gaps: 0

US-09-655-272-4 (1-370) x US-60-443-566-876 (1-3256)

QY 1 MetAlaProAspLeuLeuAspProLysSerAlaAlaGlnSerLysProArgLeu 20  
 Db 64 GTGGCGGACCTGACTTGTGGATCTTAATCTCCGCTCAGAACTCCAAACCGAGGCTC 123  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 Db 124 TCGTTTTCACGAACCCACAGTCTTCTTCCCGGTGGAGTGACGACCAATTAAT 183  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuLysLeuIle 60  
 Db 184 GTTATGAATGAGAGAGCTCTCCACGATATCTCTGGTGTGTCTCTATCTGATCATC 243  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluClnProGlnGluIleSerGlnArgThrIle 80  
 Db 244 GGAGCCACCGTGTTCAGAGCATTGGAGCAGCTCATGAGATTCACAGAGGACCACTT 303  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 304 GTGATCCAGAGCAAAACATTATATCCCAACATCTCTGTGTCAATTCGAGGAGCTGGAT 363  
 QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 364 GAATCTCATTGACAAATAGTGGCAATAAATGACGAGTATATACCTTAGGAAACACC 423  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyValIle 140  
 Db 424 TCCAATCAATCAGTCACTGGGATTTGGAAAGTCTCTTCTTCTTGTGGGACCTGTTAT 483  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 484 ACACCATAGGATTTGGAAACATCTCACCACGACAGAGGGGCAAAATATCTGTATC 543  
 QY 161 IleThrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 544 ATCTATGCTTACTGGAATTCCTCTTGTGGTCTTCTTGTGGTGGAGTGGAGATCAG 603  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 604 CTAGGCACCATATTTTGGAAAGGAATTTGCCAAAGTGGAGATACGTTTATTAAGTGGAT 663

QY 201 ValSerGlnThrLysIleArgIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 664 GTTAGTCAGACCAAGATTGCGCATCATCTCAACATCATATTTATATCTATTTGGCTGTGTA 723  
 QY 221 LeuPheValAlaLeuProAlaValIlePheIleHisIleGluGlyTrpSerAlaLeuAsp 240  
 Db 724 CTCTTTGTGGCTCTGCGCTGCGATCATATTCACATACATAGAGCTGGAGTCCCTGGAC 783  
 QY 241 AlaIleTrpPheValValIleThrLeuThrThrIleGlyPheGlyAspTrpValAlaGly 260  
 Db 784 GCCATTATTTTGGTGTATCTCACTCAACATATTCGATTTGGTGTGCTGCTGATCCTTGTGA 843  
 QY 261 GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleVal 280  
 Db 844 GGATCCGATATTGAATATCTGCACTTCTATTAAGGCTGTCTGTGTGTCTGATCCTTGTGA 903  
 QY 281 GlyLeuAlaTrpPheAlaAlaValLeuSerMetIleGlyAspTrpLeuAlaGlyValIleSer 300  
 Db 904 GGGCTTGTCTTACTTTGCTGCTGTCTGAGCAATGAGATTTGGTCCGAGTGTATCT 963  
 QY 301 LysLysThrLysGluGluValGlyLysPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320  
 Db 964 AAAAGACAAAAGAGAGTGGAGAGTTTCAGACACACGCTGCTGAGTGGACAGCAAC 1023  
 QY 321 ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTrpAspLysPhe 340  
 Db 1024 GTACAGCCGAATTCAAAGAAACCCAGGAGGAGTGTAGTGTGGAGATTTATGACAAGTTC 1083  
 QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisGln 360  
 Db 1084 CAGCGGGCCACCTCCATCAAGCGGAAGCTCTCGGAGAACTGGCTGGAAACCAACATCAG 1143  
 QY 361 GluLeuThrProCysMetArgThr 368  
 Db 1144 GAGCTGACTCTTGTAGGAGGACC 1167

RESULT 12

US-60-455-444-3496  
 ; Sequence 3496, Application US/60455444  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: BEGOVICH, Ann  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001455  
 ; CURRENT APPLICATION NUMBER: US/60/455,444  
 ; CURRENT FILING DATE: 2003-03-18  
 ; NUMBER OF SEQ ID NOS: 50986  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 3496  
 ; LENGTH: 3256  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-60-455-444-3496

Alignment Scores:  
 Pred. No.: 2,286-192 Length: 3256  
 Score: 1829.00 Matches: 355  
 Percent Similarity: 98.91% Conservative: 9  
 Best Local Similarity: 96.47% Mismatches: 4  
 Query Match: 97.13% Indels: 0  
 Gaps: 0

US-09-655-272-4 (1-370) x US-60-455-444-3496 (1-3256)

QY 1 MetAlaProAspLeuLeuAspProLysSerAlaAlaGlnSerLysProArgLeu 20  
 Db 64 GTGGCGGACCTGACTTGTGGATCTTAATCTCCGCTCAGAACTCCAAACCGAGGCTC 123  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn 40  
 Db 124 TCGTTTTCACGAACCCACAGTCTTCTTCCCGGTGGAGTGGAGATTAAT 183

Qy	41	ValMetIysTrpLysThrValSerThrIlePheLeuValValLeuTyrLeuIleIle	60
Db	184	GTATGAAATGGAAGCGGTCTCCACGATATCTCTGGTGGTGTCTCTATCTCATCATC	243
Qy	61	GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle	80
Db	244	GGAGCCACCGTGTCAAAGCATTCGAGCAGCTCATGAGATTTCCACAGAGGACCACCAT	303
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp	100
Db	304	GTGATCAGGAAGCAAAACATTCATATCCCAACATTCCTGTGTGTCAAATTCGACGGAGCTGGAT	363
Qy	101	GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer	120
Db	364	GAATCATTCAGCAAAATAGTGGCAGCAATAAATCGAGGATATTACCGTTAGGAAACACC	423
Qy	121	SerAenGlnValSerHisTrpAspLeuGlySerPhePheAlaGlyThrValIle	140
Db	424	TCCAATCAAAATCAGTCATCGGATTTGGGAAGTTCCTTCTTTGTGGCACTGTATT	483
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160
Db	484	ACAACCATAGATTTGGAAACATCTCACGACGACAGAAGYGGCAAAATATTCGTATC	543
Qy	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
Db	544	ATCTATGCCTTACTGGGAATTTCCCTCTTTGGTTTTCTCTGGCTGGAGTTGGAGATCAG	603
Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	604	CTAGGCACCATATTTGGAAAGGAATTTGCCAAGTGAAGATACGTTTATTAAGTGGAAAT	663
Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	664	GTTAGTCAGACCAAGATTGGCATCATCTCAACATCATATTTATCTATTTGGCTGTGTA	723
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	724	CTCTTTGTGGCTCTGGCTGGCATCATATCAAAACACATAGAAAGCTGGAGTGGCCCTGGAC	783
Qy	241	AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly	260
Db	784	GCCATTTATTTTGGTTATCCTCTAACAACTATTGGATTGGTGACTACGTTTGCAAGT	843
Qy	261	GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal	280
Db	844	GGATCCGATATTGGAATATCTGGACTTCTATAAGCCTGTCTGTGTGGTTCTGGATCCTTGTA	903
Qy	281	GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer	300
Db	904	GGGCTTCCTTACTTTGTCTGTCTCCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT	963
Qy	301	LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn	320
Db	964	AAAAAGACAAAAGAAGAGTGGGAGATTCCAGACACACGCTGCTGAGTGGACAGCCAAC	1023
Qy	321	ValThrAlaGluPheLysGluThrArgArgArgLeuSerValGluIleTyrAspLysPhe	340
Db	1024	GTCAAGCCGAATTTCAAAGAAACACAGAGGCGACTGAGTGTGGAGATTTTATGACAAGTTC	1083
Qy	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyValAsnHisAsnGln	360
Db	1084	CAGCGGGCCACCTCCATCAACGGGAAGCTCTCGGCAGACTCTGGCTGGAAACCAACATCAG	1143
Qy	361	GluLeuThrProCysMetArgThr	368
Db	1144	GAGCTGACTCTCTGTAGGAGACC	1167

## RESULT 13

RESULT 13  
US-60-465-241-3496

US-60-465-241-3496  
; Sequence 3496, Application US/60465241

: sequence 3436, Appl. : GENERAL INFORMATION:

```

: APPLICANT: CARGILL, Michele
:
: APPLICANT: BEGOVICH, Ann
:
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
:
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CL001468
:
: CURRENT APPLICATION NUMBER: US/60/465,241
:
: CURRENT FILING DATE: 2003-04-23
:
: NUMBER OF SEQ ID NOS: 258418
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 3496
:
: LENGTH: 3256
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-60-465-241-3496

```

Alignment Scores:		
Pred. No.:	2.28e-192	Length:
Score:	1829.00	Matches:
Percent Similarity:	98.91%	Conservative:
Best Local Similarity:	96.47%	Mismatches:
Query Match:	97.13%	Indels:
DB:	112	Gaps:
		0
		3256

US-09-655-272-4 (1-370) X US-60-465-241-3496 (1-3256)

Qy	1	MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu	20
Db	64	GTGGGGACCTGACTTGTCTGGATCCTAAATCTCGCGTCAGAACTCCAAACCGAGGCTC	123
Qy	21	SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn	40
Db	124	TGCTTTTCCACGAACCCACACAGTCTGCTTCCCGGGTGGAGAGTGACACGACCATTAAT	183
Qy	41	ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuLysTrpLeuIleIle	60
Db	184	GTTATGAATATGGAGACGGCTCTCCACGATATCTCTGGTGTTCCTCTATCTGATCATC	243
Qy	61	GlyAlaAlaValPheLysAlaLeuGlnProGlnGluLysSerGlnArgThrThrIle	80
Db	244	GGAGCCACCGTGTTCAAAGCATTTGAGCAGCGCTCATGAGATTTCACAGAGACCACCATT	303
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp	100
Db	304	GTGATCCAGAGCAACAACTCATATCCCAACATTTCTGTGTCAATTCCAGCGGAGCTGGAT	363
Qy	101	GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyLysnSer	120
Db	364	GAATCAITTCAGCAAAATAGTGGCAGCAATAAATGCAGGGATTATACCGTTAGGAAACCC	423
Qy	121	SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle	140
Db	424	TCCATCAAAATCAGTCACTGGGATTTGGGAAGTTCCCTTCTTTGTCTGGCACTGTATT	483
Qy	141	ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle	160
Db	484	ACAACCATAGGATTTGGAAACATCTCCACGCGCAGAGGCGGCAAAATATTCTGTATC	543
Qy	161	IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
Db	544	ATCTATGCTTACTGGGAATTTCCCTCTTTGGTTTTCTCTTGGCTGGAGTTGGAGATCAG	603
Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
Db	604	CTAGGCACCATATTTTGGAAAGGAATTTGCCAAAGTGGAGATACGTTTATTATGTGGAT	663
Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
Db	664	GTTAGTCAGCAACAGATTCGCATCATCTCAACATCATATTTATATCTATTTTGGCTGTGA	723
Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
Db	724	CTCTTTGTGGCTCTGCTCGCATCATATTCAACACATAGAAGCTCGGAGTGCCTCGAC	783

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QY 241 AlaileTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 784 GCCATTTATTTGGTTATCACTTAACAACACTATTGGATTGGTACACTACGTTGAGGT 843
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 844 GGATCCGATATGAATATCTGGACTCTCTAAGCCCTGCTGTGGTTCTGGATCCTTGTGA 903
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 904 GGGCTTCTTACTTGTCTGTCTGCTGAGCATGATGGAGATTGGCTCCGAGTGATATCT 963
QY 301 LysIleThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 964 AAAAAGCAAAAGAGAGTGGAGAGTTCCAGAGCACACGCTGCTGAGTGGACAGCCAAC 1023
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1024 GTCACAGCCGAATTCAAAGAAACCCAGAGCGGACTGAGTGTGAGATTTATGACAAGTTC 1083
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1084 CAGCGGCCACCTCCATCAGCGGAAGCTCTCGGCAGAACTGGCTGGAAACCAATCAG 1143
QY 361 GluLeuThrProCysMetArgThr 368
Db 1144 GAGCTGACTCTTGTAGGAGACC 1167

RESULT 14
PCT-US03-01911-9
; Sequence 9, Application PC/TUS0301911
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE OF INVENTION: USE THEREOF
; CURRENT APPLICATION NUMBER: PCT/US03/01911
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2391
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
PCT-US03-01911-9

Alignment Scores:
Pred. No.: 2,5e-192 Length: 2391
Score: 1827.00 Matches: 354
Percent Similarity: 98.91% Conservative: 10
Best Local Similarity: 96.20% Mismatches: 4
Query Match: 97.03% Indels: 0
DB: Gaps: 0

US-09-655-272-4 (1-370) x PCT-US03-01911-9 (1-2391)
QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20
Db 586 TTGGCGGCACCTGACTTGGTCTGAACTCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 645
QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
Db 646 TCGTTTTCCAGAAACCCACAGTGTCTTCTCCCGGGTGGAGGTGACACCACTTAAT 705
QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrLeuIle 60
Db 706 GTTATGAATGAAGACGGTCTCCACGATATCTCTGGTGTGTGCTCTATCTATCATC 765
QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80
```

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Db 766 GGAGCCACCGTGTTCAAAGCAATTTGGAGCAGCGCTCATAGATTTTCACAGAGCACCACTT 825
QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 826 GTGATCCAGAGCAACCAATTCATATCCCAACATTCCTGTGTCAATTCACGCGAGGTGGAT 885
QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 886 GAACCTCATTCAGCAATATAGTGGCAGCAATTAATGAGGAGTATATACCGTTAGGAACACC 945
QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 946 TCCAAATCAATCAGTCACTGGGATTTGGAAAGTTCCTTCTTCTTTCGTGGCACTGTATT 1005
QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
Db 1006 ACAACCATAGGATTTGGAAACATCTCACACGACAGAGCGGCAAAATATCTTGATC 1065
QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 1066 ATCTATGCTTACTGGGAATTCCTTCTTGGTTTCTTCTTGGCTGGAGTTGGAGATCAG 1125
QY 181 LeuGlyThrIlePheGlyGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 1126 CTAGGCACCATATTTGGAAAGGAATTCGCAAGTGGAGATACGTTTATTAAAGTGGAT 1185
QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220
Db 1186 GTTAGTCAGACCAAGATTCGCATCATCTCAACAATCATATTTATATTTGGCTGTGTA 1245
QY 221 LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp 240
Db 1246 CTCTTTGTGGCTCTGCTCGCATCATATTCAAAACACATAGAAAGGCTGGAGTCCCTGGAC 1305
QY 241 AlaIleTyrPheValValIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaGly 260
Db 1306 GCATTTATTTTGTGGTATCACTCTAACAACTATTGGATTGGTGTGACTACGTTGAGGT 1365
QY 261 GlySerAspIleGluTyrLeuAspPheTyrLysProValValTrpPheTrpIleLeuVal 280
Db 1366 GGATCCGATATTCATATCTGGACTCTATAAGCCTGCTGCTGTGTTCTGGATCCTTGTGA 1425
QY 281 GlyLeuAlaTyrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSer 300
Db 1426 GGGCTTCTTACTTGTCTGCTGCTGAGCATGATGGAGATTTGGCTCCGAGTGATATCT 1485
QY 301 LysLysThrLysGluGluValGlyGluPheArgAlaHisAlaAlaGluTrpThrAlaAsn 320
Db 1486 AAAAGCAAAAGAGAGTGGAGAGTTCAAGACACACGCTGCTGAGTGGACGCCAAC 1545
QY 321 ValThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPhe 340
Db 1546 GTCACAGCCGAATTCAAAGAAACCCAGAGCGGCTGAGTGTGGAGATTTATGACAAGTTC 1605
QY 341 GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln 360
Db 1606 CAGCGGCCACCTCCATCAAGCGGAAGTCTCGGCAGAACTCGCTGGAAACCAATCAG 1665
QY 361 GluLeuThrProCysMetArgThr 368
Db 1666 GAGCTGACTCTTGTAGGAGACC 1689
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## RESULT 15

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US-10-349-528-9
; Sequence 9, Application US/10349528
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE OF INVENTION: USE THEREOF
; FILE REFERENCE: D0210
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; CURRENT APPLICATION NUMBER: US/10/349,528
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; LENGTH: 2391
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-349-528-9

```

Alignment Scores:			
Pred. No.:	2.5e-192	Length:	2391
Score:	1827.00	Matches:	354
Percent Similarity:	98.91%	Conservative:	10
Best Local Similarity:	96.20%	Mismatches:	4
Query Match:	97.03%	Indels:	0
DB:	51	Gaps:	0

US-09-655-272-4 (1-370) x US-10-349-528-9 (1-2391)

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Db	586	TTGGCGGCACCTGACTTCTGGATCCTAAATCTGCGCTCAGAACTCCAAACCGAGGCTC	645
Qy	21	SerPheSerSerIysProThrValLeuAlaSerArgValGluSerAspSerAlaLeuAsn	40
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Db	766	GGAGCCACCGTGTCAAGCATTTGGAGCAGCCTCATGAGATTTTCACAGGGACCACTT	825
Qy	81	ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp	100
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Qy	161	IleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln	180
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Qy	181	LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn	200
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Qy	201	ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal	220
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Qy	221	LeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAsp	240
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Db	1306	GCCATTATTTTGGTGTATCACTCAACAACATATTGGATTGGTGTGATCTACGTTGCAGGT	1365
Qy	261	GlySerAspIleGluTrpLeuAspPheTrpLysProValValTrpPheTrpIleLeuVal	280

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Db	1426	GGCTTGGCTTACTTTGCTGCTGCTGAGCATGATTGGAGATTGGCTCCGAGTGATATCT	1485
Qy	301	LysLysThrLysGluGluValGlyGlyPheArgAlaHisAlaGluTrpThrAlaAsn	320
Db	1486	AAAAGACAAAAGAGAGGTGGGAGAGTTCAAAGCACACGCTCTGAGTGGACAGCCAAC	1545
Qy	321	ValThrAlaGluPheLysGluThrArgArqLeuSerValGluIleTyrAspLysPhe	340
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Qy	341	GlnArgAlaThrSerValLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGln	360
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Qy	361	GluLeuThrProCysMetArgThr	368
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 2, 2005, 21:56:31 ; Search time 3769.86 Seconds

(without alignments)

3576.449 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 65645750

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Listing first 45 summaries

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9: gb\_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1646	87.4	1113	9 AY418065	AY418065 Homo sapi
3	1252.5	66.5	1745	3 AK036066	AK036066 Mus muscu
4	1252.5	66.5	2534	3 AK082153	AK082153 Mus muscu
5	1225.5	65.1	2628	3 AK031904	AK031904 Mus muscu
6	1211	64.3	1113	9 AY418066	AY418066 Pan trogl
7	1134	60.2	713	6 CB526721	CB526721 UT-M-PYO
8	1106	58.7	920	5 BQ948206	BQ948206 AGENCOURT
9	1045	55.5	654	7 CK005597	CK005597 AGENCOURT

10	955	50.7	834	7	CO248930	CO248930 AGENCOURT
11	949	50.4	827	7	CO249404	CO249404 AGENCOURT
12	945.5	50.2	840	7	CO247814	CO247814 AGENCOURT
13	943	50.1	760	5	BU610944	BU610944 UT-M-FCO-
14	932.5	49.5	854	7	CO249306	CO249306 AGENCOURT
15	929	49.3	832	7	CO245300	CO245300 AGENCOURT
16	924.5	49.1	598	6	CF171014	CF171014 B0837A01-
17	912	48.4	537	5	BX478651	BX478651 DKF2p866H
18	911	48.4	775	7	CN528767	CN528767 UT-M-HQO-
19	876	46.5	784	5	BQ042251	BQ042251 UT-M-BQO-
20	862	45.8	869	5	BU956092	BU956092 AGENCOURT
21	817	43.4	479	6	CA871490	CA871490 K0910F08-
22	797	42.3	1182	9	AY405804	AY405804 Homo sapi
23	793	42.1	532	6	CD625302	CD625302 S5013674J
24	793	42.1	532	6	CD625313	CD625313 S5013751H
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26	793	42.1	533	6	CD625314	CD625314 S5013751J
27	790	42.0	532	6	CD625321	CD625321 S5013895H
28	787	41.8	653	6	CD625293	CD625293 S5013078H
29	784	41.6	473	6	CA890051	CA890051 B0156G04-
30	778	41.3	528	6	CD625319	CD625319 S5013886H
31	778	41.3	529	6	CD625318	CD625318 S5013878J
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33	777	41.3	530	6	CD625320	CD625320 S5013886J
34	776	41.2	533	6	CD625301	CD625301 S5013674H
35	775	41.2	533	6	CD625310	CD625310 S5013727J
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37	775	41.2	592	6	CD625296	CD625296 S5013079J
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41	767	40.7	531	6	CD625308	CD625308 S5013711J
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## ALIGNMENTS

RESULT 1	AY418067	1113 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY418067	Mus musculus KMK2 gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	AY418067	Genomic survey sequence.			
ACCESSION	AY418067.1	GI:39774027			
VERSION	GSS.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1113)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1113)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment				
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Percent Similarity: 99.39% Conservatives: 0
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Query Match: 88.32% Indels: 0
DB: 9 Gaps: 0

US-09-655-272-4 (1-370) x AY418067 (1-1113)

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QY 62 AlaAlaValPheLysAlaLeuGluInProGlnGluIleSerGlnArgThrIleVal 81
DB 61 GCCACGGTGTTCAGGCTATTGGAGCAGCTCAGAGATTTCCAGAGGACCACTTGTG 120
QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101
DB 121 ATCCAGAAGCAGACCTTCATAGCCCGACGATGCTGGCTCAACTCCACCGAGCTGGACGAA 180
QY 102 LeuIleGlnGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121
DB 181 CTATCCAGCAATATAGTGGGAGCAATATACGAGGATATATCCCTTAGGAACAGCTCC 240
QY 122 AsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIleThr 141
DB 241 AATCAAGTTAGTCACTGGGACCTCGGAAGCTCTTCTTCTTCTTGTGTACTGTATCACA 300
QY 142 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyIlePheCysIleIle 161
DB 301 ACCATAGATTGGAAACATCTCCCCAGCACTGAAGTGGAAATATATTCGTCATCATC 360
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QY 182 GlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsnVal 201
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DB 481 AGTCAGACGAAGATTCGTATCATCTCCACCATCATCTTCATCTCTGTTGGCTGTCTCTC 540
QY 222 PheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAspAla 241
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QY 242 IleTyrPheValValIleThrIleuThrThrIleGlyPheGlyAspTyrValAlaGlyGly 261
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QY 322 ThrAlaGluPheLysGluThrArgArgLeuSerValGluIleTyrAspLysPheGln 341
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RESULT 2
LOCUS AY418065 1113 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens KCN2 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY418065
VERSION AY418065.1 GI:39774025
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1113)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1113)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN

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Query Match: 87.41% Indels: 0
DB: 9 Gaps: 0

US-09-655-272-4 (1-370) x AY418065 (1-1113)

QY 42 MetLysTrpLysThrValSerThrIlePheLeuValValLeuTyrLeuIleIleGly 61
DB 1 ATGAATGGGAAGACAGTCTCCAGATTTCTGGTGTCTCTACCTGATCATCGGA 60
QY 62 AlaAlaValPheLysAlaLeuGluInProGlnGluIleSerGlnArgThrIleVal 81
DB 61 GCCACGGTGTTCAGGCTATTGGAGCAGCTCAGAGATTTCCAGAGGACCACTTGTG 120
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DB 121 ATCCAGAAGCAGACCTTCATAGCCCGACGATGCTGGCTCAACTCCACCGAGCTGGACGAA 180
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DB 301 ACCATAGATTGGAAACATCTCCCCAGCACTGAAGTGGAAATATATTCGTCATCATC 360
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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

#### JOURNAL MEDLINE PUBLISHED REFERENCE

20530913  
11076861

#### AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

#### AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

#### AUTHORS

6 (bases 1 to 2534)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyahashi, A., Yaeunishi, A., Muraatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

#### COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

#### FEATURES

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/notes="unnamed protein product; POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog [Rattus norvegicus] (SWISSPROT|Q9JIS4, evidence: FASTA, 99.4%ID, 97.2%length, match=1569) putative"
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#### CDS

#### ORIGIN

Alignment Scores:

Pred. No.: 2,15e-142 Length: 2534  
Score: 1252.50 Matches: 247  
Percent Similarity: 79.58% Conservative: 53  
Best Local Similarity: 65.52% Mismatches: 66  
Query Match: 66.52% Indels: 11  
DB: 3 Gaps: 5

US-09-655-272-4 (1-370) x AK082153 (1-2534)

QY 2 AlaAlaProAspLeuLeuAspProLysSerAla-----AlaGlnAnSerLysProArg 19

Db 171 GCAGCCCCCAGTGTGCCAGGCCAAGAGTGCCTAACGGGCATCACCTGTCTCTCGA 230

QY 20 LeuSerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSer----- 37

Db 231 CTCTCCATTCTCTCGAGCCACGGTGTAGCC---AGGATGGGAAGCGCCTCCACAGGA 287

QY 38 ---AlaIleAsnValMetLysTrpLysThrValSerThrIlePheLeuValValLeu 56

Db 288 GGCCTGCAACAGTATGAAGTGGAAACAGGTGGTCCCATCTTGTGTGGTGTGGTGC 347

QY 57 TyrLeuIleIleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnIleSerGln 76

Db 348 TACCTCGTCACTGGTGGCTTGTCTTCGGCGCTTGGAAACAGCCCTTCGAGAGCAGT 407

QY 77 ArgThrThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAnSer 96

Db 408 AAGAACACAACTCGCTTGGGAAGGCAGAAATCTTTCAGAGATCACATCTGTGTGAGTCC 467

QY 97 ThrGluLeuAspGluLeuIleGlnIleValAlaIleAsnAlaGlyIleIlePro 116

Db 468 CAGGAACCTAGACACTGATTTCAGCATCGCTGCTGTATACCGGGAGTGCAGCCCA 527

QY 117 LeuGlyAsnSerSerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAla 136

Db 528 GTAGGAACACTCTTCCAACAGCAGCAGTCACTGGACCTTGGAAAGTGCCTTCTTCTT 587

QY 137 GlyThrValIleThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLys 156

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Db 947



QY 57 TyrllellelleGlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGln 76  
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 QY 77 ArgThrThrIleValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSer 96  
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 QY 97 ThrGluLeuAspGluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIlePro 116  
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 QY 336 IleTrpAspLysPheGlnArgAlaThrSerVal-----LysArgLysLeuSer 351  
 Db 1118 ATCCATGACAGCTGCAACGGGCGACCATCTCCGAGATGATGAGCGCGAGGCTGGC 1177  
 QY 352 AlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrProCysMetArgThr 368  
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 LOCUS Pan troglodytes KCN2 gene, VIRUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY418066  
 VERSION AY418066.1 GI:39774026  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 1113)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1113)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 FEATURES  
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 gene <1..->1113  
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 /locus\_tag="HCM6433"  
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 Alignment Scores: 7.89e-138 Length: 1113  
 Pred. No.: 1211.00 Matches: 237  
 Score: 91.32% Conservative: 5  
 Percent Similarity: 89.43% Mismatches: 23  
 Best Local Similarity: 64.31% Indels: 0  
 Query Match: 9  
 DB: 0  
 US-09-655-272-4 (1-370) x AY418066 (1-1113)  
 QY 42 MetLysTrpLysThrValSerThrIlePheLeuValValLeuTyrLeuIleIleGly 61  
 Db 1 ATGAATGGAAGACGGTCTCCAGATATTCCTGGTGTTCCTCTATCTGATCATCGA 60  
 QY 62 AlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIleVal 81  
 Db 61 GCCACCGTGTTCAAACATTTGGAGCAGCTCATGAGATTTCCAGAGGACCACCATTTG 120  
 QY 82 IleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAspGlu 101  
 Db 121 ATCCAGAAGCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGGAGCTGGATGA 180  
 QY 102 LeuIleGlnIleValAlaIleAsnAlaGlyIleIleProLeuGlyAsnSerSer 121  
 Db 181 CTCATTGAGCAATAGTGGCAGCAATAATGCGAGGATTATACCGTTAGGAAACACCTCC 240  
 QY 122 AsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIleThr 141  
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 QY 142 ThrIleGlyPheGlyAsnIleSerProArgThrGluGlyLysIlePheCysIleIle 161  
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 Db 361 TATGCTTACTGGGAATTCCTCTTTGTTGTTTCTCTTGGCTGGAGTTGGAGATCAGCTA 420  
 QY 182 GlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsnVal 201  
 Db 421 GGCACCATATTTGGAAGAGGAATTGCCAAGTGGAGATACGTTTATTAAAGTGAATGTT 480

is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

202 SerGlnThrIysleArglleSerThrIlellePheIleLeuPheGlyCysValleu 221  
 481 AGTCAGACCAAGATTCGATCATCTCAACAATCATATTTATATCTTTGGCTGTGTACTC 540  
 222 PheValAlaLeuProAlaValIlePheIleHsIleGluGlyTrpSerAlaLeuAspAla 241  
 541 TTTGTGGCTCTGCTCGATCATATTAACAACATAGAGCTGGAGTGCCTGGANNWN 600  
 242 IleTy-PheValValIleThrLeuThrThrIleGlyPheGlyAspTyrrValAlaGlyGly 261  
 601 NNN 660  
 262 SerAspIleGluTyrrLeuAspPheTyrrLysProValValTrpPheTrpIleLeuValGly 281  
 661 TCCGATATTCATATCTGGACTTCTATAAGCCCTGCTGTGGTCTCGATCTTTGAGG 720  
 282 LeuAlaTyrrPheAlaAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSerLys 301  
 721 CTTCCTTACTTTGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATA 780  
 302 LysThrLysGluGlu 306  
 781 AAGCAAAAGAGAG 795

RESULT 7  
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 IMAGE:6848897 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 NIH-MGC http://mgc.nci.nih.gov/  
 Contact: Robert Strausberg, Ph.D.  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mousefl.html  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP).

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 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail

ORIGIN

Alignment Scores:  
 Pred. No.: 1,23e-128 Length: 713  
 Score: 1134.00 Matches: 227  
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 Best Local Similarity: 99.13% Mismatches: 1  
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 DB: 6 Gaps: 0  
 US-09-655-272-4 (1-370) x CB526721 (1-713)  
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 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 Db 85 TCATTCTCTCTCAAAACCCACCGTCTTCTTCCCGGTGGAGAGTACTCGGCCATTAT 144  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrrIleIle 60  
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 QY 61 GlyAlaAlaValPheIysAlaLeuGluGlnProGlnGlnIleSerGlnArgThrThrIle 80  
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 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAlaAlaGlyIleIleProleuGlyAsnSer 120  
 Db 325 GAACTCATCCAGCAATAGTGGCAGCAATAACCGAGGAGTATCCCTTAGGAACACAGC 384  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
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 QY 161 IleTyrrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
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 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 565 CTAGGAACATATATTGGAAGAAGATTCGAAGGTGGAGACACATTTATTAAAGTGAAT 624  
 QY 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCysVal 220  
 Db 625 GTTAGTCAGACGAAAGATTCGATCATCTCCACCATCATCTTCTCTGTTGGCTGTGTC 684  
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RESULT 8  
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 LOCUS  
 DEFINITION  
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 5', mRNA sequence.  
 ACCESSION  
 VERSION  
 BQ948206.1  
 GI:22363684  
 EST.

SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 920)  
NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Susan L. Sullivan, phd.  
CDNA Library Preparation: ResGen, Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM13879 row: c column: 09  
High quality sequence start: 18  
High quality sequence stop: 553.  
Location/Qualifiers  
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Primer: Oligo dt. Average insert size 2.2 Kb. Constructed  
by ResGen, Invitrogen Corp. Note: this is a NIH\_MGC  
Library."  
ORIGIN  
Alignment Scores:  
Pred. No.: 5.16e-125 Length: 920  
Score: 1106.00 Matches: 217  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 1  
Query Match: 58.74% Indels: 1  
DB: 5 Gaps: 0  
US-09-655-272-4 (1-370) x BQ948206 (1-920)  
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Qy 166 YIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGlnLeuGlyThrIlePheG1 186  
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Qy 186 YLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsnValSerGlnThrIlysl 206  
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Qy 226 oAlaValIlePheLysHisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheValva 246  
Db 245 TGGGTATATTCAAGCACATAGAGGCTGGAGCGCTGGAGCGCTGCATCTATTTTGGGT 304  
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286 aAlaValLeuSerMetIleGlyAspTrpLeuArgValIleSerLysIlysrThrIlyslGluG1 306  
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Qy 306 uValGlyGluPheArgAlaHisAlaAlaGluTTrpThrAlaAsnValThrAlaGluPheLy 326  
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Db 545 GGAACACGAGGAGCGGCTGAGCTGAGATCTACGACAAAGTTCAGGCTCCACATCCGT 604  
Qy 346 lLysArgLysLeuSerAlaGluLeuAlaGlyAsnHisAsnGlnGluLeuThrPro 364  
Db 605 GAAGCGGAAACTCTCCGAGAGCTGGCGGCAAAACACCAACGAGAACTGACTCCG 659

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LOCUS  
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DEFINITION  
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IMAGE:30721772 5', mRNA sequence.  
ACCESSION  
CK005597  
VERSION  
CK005597.1 GI:38531639  
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EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 654)  
NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapsb-r@mail.nih.gov  
Tissue Procurement: Professor Miklas Palkovits  
CDNA Library Preparation: Michael Brownstein / Ted Usdin  
Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDCM270 row: f column: 21  
High quality sequence stop: 585.  
Location/Qualifiers  
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/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC 229"  
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oligo-dT primed and directionally cloned.5' and 3'  
adaptors were used in cloning as follows:  
5'-AAGCAGTGGTATCAACGAGATGGCGCATTCAGCGCGG-3'-ATTCTAGAGG  
CCGAGCGCCGACATG-d(T)3N-IN-3. Full-length enriched  
library was constructed using the Clontech Creator SMART  
kit and size-selected for >0.5kb with an average insert  
size of 1.2kb Library created in the laboratory of  
Jonathan Kuo and Ted Usdin."

Alignment Scores:  
Pred. No.: 1.01e-117 Length: 654  
Score: 1045.00 Matches: 208  
Percent Similarity: 98.16% Conservative: 5  
Best Local Similarity: 95.85% Mismatches: 4







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 Db 467 ACAACCATAGGATTGGAAACATCTCCACGACGACAGAGCGGCGCAAAATATTCTGTATC 526  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 527 ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTTGGCTGGAGTTGGAGATCAG 586  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200  
 Db 587 CTAGGCACCATATTGGAAAGGATT-GCCAAAGTGAAGATCG-TTATTAAAGTGAAT 644  
 QY 201 ValSerGlnThrIleLysIleArgIle-----IleSerThrIleIlePheIleLeuPheGly 218  
 Db 645 GTTAGTCAGACCAAGAT-CGCACTCCCAACATATTAACTATTGTGGTGGTACCTGGGCC 703  
 QY 219 CysValLeuPhe-----ValAlaLeuProAlaValIlePheLysHisIleGluGly 235  
 Db 704 TGTGCAATTACACCTAAAGCTGATGCTGACCATATTGTGTACCCACACATGATTGGA 763  
 QY 236 TrpSerAlaLeuAspAlaIleTyrPheVal 245  
 Db 764 ACNTGGCGATCATGAACGATATAGCGGTC 793

## RESULT 11

CO249404  
 LOCUS  
 DEFINITION AGENCOURT 25900989 NIH MGC 195 Homo sapiens cDNA clone  
 IMAGE:7286364 5', mRNA sequence.  
 ACCESSION CO249404  
 VERSION CO249404.1 GI:49120300  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 827)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: IRBK8 row: g column: 10  
 High quality sequence start: 15  
 High quality sequence stop: 639.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:7286364"  
 /tissue\_type="mixed"  
 /lab\_host="DH5A (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 195"  
 /note="Vector: pDNR-Dual; Site 1: loxp-Salt; Site 2:  
 loxp-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxp sites

## FEATURES

source  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:7286364"  
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 /lab\_host="DH5A (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 195"  
 /note="Vector: pDNR-Dual; Site 1: loxp-Salt; Site 2:  
 loxp-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxp sites

of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores: 9.86e-106 Length: 827  
 Score: 949.00 Matches: 201  
 Percent Similarity: 85.43% Conservative: 16  
 Best Local Similarity: 79.13% Mismatches: 22  
 Query Match: 50.40% Indels: 17  
 DB: 7 Gaps: 3  
 US-09-655-272-4 (1-370) x CO249404 (1-827)  
 QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 Db 46 ATGGCGGCACCTGACCTTGGTATCTAAATCTGCCGCTCAGAACTCCAAACCGAGGCTC 105  
 QY 21 SerPheSerSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40  
 Db 106 TCGTTTTCCAGAAACCCACAGTGTCTGCCGGGTGGAGAGTGACACGACCATTAAT 165  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValLeuValLeuIle 60  
 Db 166 GTTATGAATGGAAGACGGTCTCCAGATATTCCTGGTGTCTCTATCTGATCATC 225  
 QY 61 GlyValAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 Db 226 GGAGCCACCGTGTTCAGACATTTGGAGAGCCTCATGAGATTTTCACAGAGACCCACTT 285  
 QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 286 GTGATCCAGAAAGCAAAACATTCATATCCCAACATTCCTGTGTCAATTCGACGAGCTGGAT 345  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 346 GAACTCATTCAGCAATATAGTGGCAGCAATAATGACAGGATTAATCCGTTAGGAACACC 405  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140  
 Db 406 TCCATCAATCAATCAGTCACCTGGGATTTGGAGAGTTCTCTCTCTTCTGCTGGCACTGTATT 465  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 466 ACAACCATAGGATTTGGAAACATCTCCACGACGACAGAAAGCGGCAAAATATTCTGTATC 525  
 QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 526 ATCTATGCTTACTGGGAATCCCTCTTTGGTTTCTTGGCTGGAGTTGGAGATCAG 585  
 QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPhe----- 196  
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 QY 197 IleLysTrpAsnValSerGlnThrIleLysIleArgIleIleSerThrIleIlePheIleLeu 216  
 Db 645 ATCAGACCAAAATTCCTCT-----CTCAACACTATTATCTATTG-CTG 685  
 QY 217 PheGlyCys-----ValLeuPheValAlaLeuProAlaValIlePheLys 231  
 Db 686 GTACCTTGGCTGTGCTGCACTATCACATAAGCTGATGCTGAGCATATTGTGTATCCA 745  
 QY 232 HisIleGluGlyTrpSerAlaLeuAspAlaIleTyrPheVal 245  
 Db 746 CACATATGGACACTCGGTCAATGATCGACTACGCGGTG 787

RESULT 12

CO247814 840 bp mRNA linear EST 23-JUN-2004  
 LOCUS AGENCOURT 25900957 NIH\_MGC\_195 Homo sapiens cDNA clone  
 DEFINITION IMAGE:7286362 5', mRNA sequence.  
 CO247814  
 ACCESSION CO247814.1 GI:49114558  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 840)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: IRB8 row: 9 column: 08  
 High quality sequence start: 18  
 High quality sequence stop: 627.  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:7286362"  
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 /lab\_host="DH5A (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 195"  
 /note="vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC Library."

US-09-655-272-4 (1-370) x CO247814 (1-840)

Alignment Scores:  
 Pred. No.: 2.73e-105 Length: 840  
 Score: 945.50 Matches: 198  
 Percent Similarity: 86.69% Conservative: 17  
 Best Local Similarity: 79.84% Mismatches: 26  
 Query Match: 50.21% Indels: 8  
 DB: 7 Gaps: 3

US-09-655-272-4 (1-370) x CO247814 (1-840)

QY 1 MetaLaAProAspLeuLeuAspProLysSerAlaAlaGlnAsnSerLysProArgLeu 20  
 Db 48 ATGGCGGCACTGACTTCTGGATCTTAATCTCGCGCTCAGACTCCAAACCGGCTC 107  
 QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaAlaAsn 40

Db 108 TCGTTTCCAGAAACCCAGAGTCTTCTCCCGGGTGGAGAGTACACACCATTAAT 167  
 QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuLysLeuIle 60  
 Db 168 GTTATGAATGGAACGCTCTCCAGATATCTCTGGTGGTGTCTCTATCTGATCATC 227  
 QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrIle 80  
 Db 228 GGAGCCACCGTGTTCAAAGCATTTGGAGCAGCTCATGAGATTTTCACAGAGGACCACT 287  
 QY 81 VallieGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100  
 Db 288 GTGATCCAGAACCAACATTCATATCCCAACATCTCTGTGCAATTCACAGGAGCTGAT 347  
 QY 101 GluLeuIleGlnGlnIleValAlaAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120  
 Db 348 GAACCTCATTCCAGCAATAGTGGCAGCAATTAATCAGGAGTATATACCGTTAGGAACACC 407  
 QY 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValle 140  
 Db 408 TCCAATCAATCAGTCACTGGGATTTGGAAAGTTCCTTCTTTCTGGTGGCACTGTATT 467  
 QY 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160  
 Db 468 ACARCCATAGGATTTGGAAACATCTCACAGCAGCAAGCGGCAAAATATCTGTATC 527  
 QY 161 IleTyraAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180  
 Db 528 ATCTATGCTTACTGGGAATTCCTCTTGGTTCCTTCTGGTGGAGTTGGAGATCAG 587  
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 Db 644 GTATCAGAC---CAATCGCTCATCTCAACACATTAATCTATGCTGGTATCTTGTGCC 700  
 QY 220 -----ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGly 235  
 Db 701 TGCTGCTTATCACACTAAAGCTGATGCTGAGCATTTATTTGTACCCACACATGATGGA 760  
 QY 236 TrpSerAlaLeuAspAlaIleTyr 243  
 Db 761 CACTGCGGATCATGAACGATCTAC 784

RESULT 13  
 BU610944 760 bp mRNA linear EST 20-FEB-2003  
 LOCUS UI-M-FCO-cas-e-02-0-UI-r1 NIH\_BMAP\_FCO Mus musculus cDNA clone  
 DEFINITION UI-M-FCO-cas-e-02-0-UI 5', mRNA sequence.  
 ACCESSION BU610944  
 VERSION BU610944.1 GI:23277159  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 760)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

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FEATURES
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    Location/Qualifiers
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        /mol_type="mRNA"
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        /db_xref="taxon:10090"
        /clone="UI-M-FCO-cas-e-02-0-UI"
        /tissue_type="whole brain"
        /dev_stage="embryo 12.5 dpc"
        /lab_host="DH10B (TI phage resistant)"
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        /notes="Organ: brain; vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Alignment Scores:
Pred. No.:      4.75e-105      Length:      760
Score:          943.00      Matches:      190
Percent Similarity: 97.45%      Conservative: 1
Best Local Similarity: 96.94%      Mismatches: 5
Query Match:     50.08%      Indels:      0
DB:              5          Gaps:          0

US-09-655-272-4 (1-370) x BU610944 (1-760)

QY 1 MetAlaAlaProAspLeuLeuAspProLysSerAlaAlaGlnAenSerLysProArgLeu 20
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QY 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAsn 40
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QY 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTyrlleIle 60
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Db 292 GTTATGAAATGGGAAGACAGTCTCCACGATTTTCTGGTGTGCTCTACCTGATCATC 351

QY 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluIleSerGlnArgThrThrIle 80
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Db 352 GGAGCCACGGTGTTCAGGCGATTTGGAGCACCTTCAGGAGATTTCCTCCAGGACCACTT 411

QY 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAenSerThrGluLeuAsp 100
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Db 412 GTGATCCAGAAGCAGACACTTCATAGCCCGACATGCTCGCTCAACTCCACCGAGCTGGAC 471

QY 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAenSer 120
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QY 141 ThrThrIleGlyPheGlyAenIleSerProArgThrGluGlyGlyIlePheCysIle 160
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Db 592 ACAACCATAGATTGTTGAAACATCTCCCCAGCACTGAAGTGGAAAAATATTCGTCATC 651

QY 161 IleTyrlAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
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Db 652 ATCTATGCCCTTCTGCTGGGAATTCNCCTCTTGGCTTTCTACTGCTGGGTGTGTGATCAG 711

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RESULT 14
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LOCUS
DEFINITION
  CO249306 854 bp mRNA linear EST 23-JUN-2004
  IMAGE:7286360 5', mRNA_sequence.
ACCESSION
  CO249306
VERSION
  CO249306.1 GI:49120079
KEYWORDS
  EST.
ORGANISM
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 854)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Narayan Bhat
  CDNA Library Preparation: Bhat Laboratory
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: IRBK8 row: g column: 06
  High quality sequence start: 17
  High quality sequence stop: 584.

FEATURES
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      /mol_type="mRNA"
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      /tissue_type="mixed"
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      /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
      loxP-HindIII; Clones from this library have been
      PCR-amplified using gene-specific primers to contain the
      complete open reading frame (based on known gene sequences
      available from NCBI's RefSeq). Template for PCR is cDNA
      derived from either pooled cytoplasmic polyA RNA from 30
      cells lines or pooled total RNA from 10 different tissues
      (from BD Biosciences/clontech and Washington University).
      PCR products are directionally cloned into the loxP sites
      of the pDNR-Dual vector. Library constructed by Dr.
      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
      Expression Laboratory, Research Technology Program, SAIC
      Frederick, NCI-Frederick, Frederick, MD 21702). For
      information on which gene each clone represents, please
      visit our anonymous ftp site at
      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
      a Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1.12e-103      Length:      854
Score:          932.50      Matches:      190
Percent Similarity: 91.07%      Conservative: 14
Best Local Similarity: 84.82%      Mismatches: 17
Query Match:     49.52%      Indels:      4
DB:              7          Gaps:          2

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US-09-655-272-4 (1-370) x C0249306 (1-854)

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Db 48 ATGGCGCACCTGACTGCTGGATCTTAATCTGCGCTCAGAACTCCAAACCGAGGCTC 107
Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAen 40
Db 108 TCGTTTTCCAGAAACCCAGAGCTGCGCTCCCGGGTGAGAGTGACACCACTTAAT 167
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTrpLeuIle 60
Db 168 GTTATGAATGGAAGCGGCTCCACGATATCTCTGGTGTGCTCTCTATCTGATCATC 227
Qy 61 GlyAlaAlaValPheLysAlaLeuGluGlnProGlnGluLeuSerGlnArgThrIle 80
Db 228 GGAGCCACCGTGTTCAAAGCAATGGAGCAGCTCATGAGATTTCCAGAGGACCACTT 287
Qy 81 ValIleGlnLysGlnThrPheIleAlaGlnHisAlaCysValAsnSerThrGluLeuAsp 100
Db 288 GTGATCCAGAAAGCAACATTCATATCCCAACATTCCTGTGTCAATTCGACGAGCTGGAT 347
Qy 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
Db 348 GAACCTATTGACCAATAGTGGCAGCAATAAATGCGGATTTATACCGTTAGGAAACACC 407
Qy 121 SerAsnGlnValSerHisTrpAspLeuGlySerSerPhePheAlaGlyThrValIle 140
Db 408 TCCAAATCAATCAGTCACTGGGATTTGGGAAGTTCCTTCTTGTGTCGACTGTATT 467
Qy 141 ThrThrIleGlyPheGlyAsnIleSerProArgThrGluGlyGlyLysIlePheCysIle 160
Db 468 ACAACCATAGATTTGGAACATCTCCACGACACAGAGCGGCAAAATATTCGTGATC 527
Qy 161 IleTrpAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db 528 ATCTATGCTTACTGGGAATTCCTCTCTTGGTGTGCTTGGTGGAGTTGGAGATCAG 587
Qy 181 LeuGlyThrIlePheGlyGlyGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
Db 588 CTAGCACCATATTGGAAAAGGATTCGCAATGGAAGA---TCGTTTATTAGTGGAT 644
Qy 201 ValSerGlnThrLysIleArgIleIleSerThrIleIlePheLeu-----PheGly 218
Db 645 GTTAT-CAGACCAATTCGCTCTCTCACACATATTAACTATTGCTGGTACCTGGGCC 703
Qy 219 CysValLeuPhe 222
Db 704 TGCTGCATCTAT 715
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ACCESSION C0245300
VERSION C0245300.1 GI:49108244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 832)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRBK8 row: 9 column: 09  
High quality sequence start: 16  
High quality sequence stop: 628.

FEATURES  
Location/Qualifiers  
1..832  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:7286363"  
/tissue\_type="mixed"  
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/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
a Note: this is a NIH\_MGC library."

ORIGIN

Alignment Scores:  
Pred. No.: 2,91e-103 Length: 832  
Score: 929.00 Matches: 196  
Percent Similarity: 86.99% Conservatives: 18  
Best Local Similarity: 79.67% Mismatches: 28  
Query Match: 49.34% Indels: 6  
DB: 7 Gaps: 1

US-09-655-272-4 (1-370) x C0245300 (1-832)

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Qy 21 SerPheSerLysProThrValLeuAlaSerArgValGluSerAspSerAlaIleAen 40
Db 106 TCGTTTTCCAGAAACCCAGAGCTGCTTCCCGGGTGAGAGTGACACCACTTAAT 165
Qy 41 ValMetLysTrpLysThrValSerThrIlePheLeuValValValLeuTrpLeuIle 60
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Qy 101 GluLeuIleGlnIleValAlaAlaIleAsnAlaGlyIleIleProLeuGlyAsnSer 120
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QY 161 IleTyrAlaLeuLeuGlyIleProLeuPheGlyPheLeuLeuAlaGlyValGlyAspGln 180
Db |||||
526 ATCTATGCCCTTACTGGGAATCCCTCTTTGGTTTCTCTGGCTGGAGTTGGAGATCAG 585
QY 181 LeuGlyThrIlePheGlyLysGlyIleAlaLysValGluAspThrPheIleLysTrpAsn 200
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586 CTAGGCACCATATTGGAAAGGATTGC--CAAGTGAAGATACTTTATTAG--TGAAT 641
QY 201 ValSerGln-ThrLysIleArgIleIleSerThrIleIlePheIleLeuPheGlyCys-- 219
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642 GTATCAGACCAAAATCGCTCTCTCACATCTATTACTATTGGTGTACCTTGTGCTGCTG 701
QY 220 -----ValLeuPheValAlaLeuProAlaValIlePheLysHisIleGluGlyTrpSe 237
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702 CATTATCACACTAAAGCTGATGTGAGCTTTATTGTGTACCCACACATGATTGGCACNTC 761
QY 237 rAlaLeuAspAlaIle 242
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762 AGCACAAGATACGATC 777
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